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TITLE: The Role of Dioxin Receptor in Mammary Development and Carcinogenesis

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14. ABSTRACT This research is testing the hypothesis that the dioxin receptor (AhR) plays a central role in breast carcinogenesis. Following on preliminary observations of the dramatic up-regulation of AhR in advanced human breast carcinoma (HBC) cell lines, we addressed whether the overexpression of the AhR alone is sufficient to induce carcinogenic transformation in mammary epithelial cells. Overexpression of AhR in clones correlated with decrease in population doubling times subsequent to abrogation to cell cycle, enhanced motility and increased migration. Furthermore, these clones acquired the ability to invade matrigel matrix and to form colonies in soft agar. Conversely, retrovirus vectors producing siRNAs targeted against AhR were used to generate stable clones with a knockdown of 75- 90% in AhR expression. Although these clones exhibited subsequent suppression of AhR-transcriptional activity, they showed no change from the vector control clone or parent cells in population doubling times, cell cycle distribution, ability to invade matrigel matrix or to form colonies in soft agar. These results suggest that AhR alone is capable of inducing transformation of immortalized normal mammary epithelial cells into a malignant phenotype, but its depletion is insufficient to reverse the malignant phenotypes in metastatic breast cancer cells. More research is required to delineate the mechanisms of AhR involvement in breast cancer progression.					
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Introduction

The proposed research studies are based on our novel observation that in three different sets of human breast carcinoma (HBC) cell lines the expression of the Aryl hydrocarbon receptor (AhR) protein was upregulated in a direct correlation with the progression of tumorigenicity. The overall objective is to determine the role of AhR in human breast carcinogenesis. AhR which is well known for its mediation of the toxic responses to environmental polyhalogenated aromatic hydrocarbons (PAH) such as dioxin (1), is a cytosolic protein and binding of PAH leads to its activation to a nuclear transcription factor and subsequent down-regulation by proteolysis (2,3,4).

Molecular cloning and characterization of AhR cDNA has identified it as a member of family of ligand-activated basic helix loop helix (bHLH) transcription factors (5). PAH-activated AhR heterodimerizes with its partner AhR nuclear translocation protein (ARNT) another bHLH transcription factor and induces the expression of a number of genes, including cytochrome P4501A1 (CYP1A1) and CYP1B1 (reviewed in 6 & 7). No endogenous ligand for the AhR has yet been identified, however, its constitutive activation via disturbing cellular adhesion to the extra-cellular matrix (8,9), increasing intracellular Ca^{2+} (10), and disturbing cytoskeleton (11) has provided evidence for physiologically activated pathways linked to adhesion. Furthermore, other lines of evidence are gathering to implicate the AhR in normal development and tissue homeostasis. For instance, TCDD exposure in animals induces teratogenesis, immunosuppression, reproductive defects and tumor promotion, in an AhR-dependent manner. The dioxin-dependent activation of the AhR has also been linked to inhibition of proliferation in mammary and uterine tumor cell lines (reviewed in 12), and enhanced terminal differentiation in keratinocytes and palatal epithelia (13,14). Moreover, the AhR null mice generated by two independent laboratories are normal and fertile, exhibiting a spectrum of hepatic and immune system defects (15,16), but are resistant to benzo(a)pyrene-induced skin and liver carcinogenicity (17). In cultured cells, TCDD shows marked effects on cell cycle progression, where it induced a cell cycle arrest at G1/S check point, an effect that is mediated through the AhR and it involves the induction of cyclin-dependent kinase (CDK) inhibitor p27^{kip1}. The AhR in absence of dioxin or other ligands, was shown to influence cell cycle progression, cell shape and differentiation (18, 19). This effect on the cell cycle progression relies on a direct protein-protein interaction of AhR with retinoblastoma (Rb) through an LXCXE domain on the AhR (20). However, studies in MCF-7 showed that AhR associates with Rb only after receptor activation and nuclear translocation (21). Furthermore, this interaction with Rb protein is required for the maximal AhR transcriptional activity (22). Although TCDD acting through AhR is a potent tumor promoter in mouse skin and in rat liver, it has strong anti-mitogenic effect in estrogen-responsive tissues and exhibits a broad spectrum of anti-estrogenic activities in human breast carcinoma cells (reviewed in 12). The AhR-null mouse or normal mouse treated with TCDD, exhibited impaired development of mammary gland ductal branching (23). Taken together with the anti-mitogenic effect exerted by TCDD on these cells, and the fact that TCDD down-regulates the AhR subsequent to its activation, these findings suggests that AhR is involved in regulating the proliferative stage required for mammary gland development. Preliminary investigations in our laboratory have demonstrated the expression of high levels of AhR protein in human mammary carcinoma cell lines in direct proportion to their degree of tumorigenicity and metastatic potential (24). We hypothesize that the AhR plays a major role in regulating mammary epithelial network during mammary gland development, and its over-expression contributes to the development of

metastatic phenotypes in human breast carcinoma. The initial aim of this work has been to investigate the mechanisms of AhR involvement in regulating mammary epithelia both during development and tumorigenesis.

Body

Progress Year 4

A fourth year was requested (without cost) in the hope of finishing some of the proposed experiments on the knockout mice (Objective 1). However, the breeding difficulty of these mice made it impossible to accomplish this goal.

Objective 1: Restoration of the normal mammary development in the AhR-KO mice by transfecting AhR cDNA into their mammary tissues *in situ* using retroviral expression vectors

This objective was partially fulfilled, however the difficulty in breeding the AhR knockout mice hampered and prevented the accomplishment of this objective, as we outlined in progress reports for years two and three (June 2004 and June 2005). We have requested the last year extension in order to continue the breeding attempts to obtain enough number of AhR^{-/-} pups for the reconstitution experiments. However these were futile attempts and we could not manage to get enough mice for the viral injection or the few that we injected have died before they reached the developmental stage for collecting mammary glands. As we reported previously (Report 2 in June 2004), we were successful in accomplishing task 1 by generating the retroviral expression vectors for both mouse and human cDNA and producing high titer viruses from each. These viruses are stored at -80°C and they will be one of the laboratory resources, which will be useful tools for other projects in our laboratory involving the murine and human AhR. Tasks 3, 4, 5, and 6 of this objective were all completed as outlined in Report 2 in June 2004.

Objective 2: To determine the status of the AhR activation in the Sager's cells in presence or absence of TCDD treatment.

This objective was successfully completed and a manuscript containing the data was submitted to a cancer research journal, however the manuscript was returned requesting analysis of more human breast carcinoma cell lines used in the field. These analyses were finished and the results were presented at the annual meeting of the American Association for Cancer Research this past April (Abstract in appendix). A revised manuscript containing the new data is being prepared to be resubmitted in the near future.

Objective 3: Over-expression of AhR in normal immortalized human mammary epithelial cells.

Objective 5: Characterization of transformed cell lines generated in Objectives 3 for their tumorigenic and invasive phenotypes.

As we reported in last year progress report this objective was successfully finished. This last year a manuscript containing the data generated was submitted to the journal of "Breast Cancer Research" and a revised version which addressed the reviewers' concerns was recently submitted and awaiting a response (pre-print is attached as an appendix).

Objective 4: Blocking of AhR expression in highly metastatic Sager's 21MT2 human breast carcinoma cell line by stably transfecting AhR siRNAs.

Objective 5: Characterization of transformed cell lines generated in Objectives 4 for their tumorigenic and invasive phenotypes.

These objectives were accomplished, as reported in last year progress report (June 2005). The details of the experiments and the results of the analyses were explained extensively in that report.

Key Research Accomplishments

- Obtaining of data to support our hypothesis that over-expression of AhR is sufficient for transformation of human mammary epithelial cells to malignant stages.
- Data obtained point to AhR as a potential target for therapeutic intervention for breast cancer.

Reportable Outcomes

- Development of retroviral expression vectors and production of retroviruses expressing genes for both human and mouse AhR.
- Development and banking of Phoenix packaging cells stably producing high titer AhR viruses
- Demonstration of the capability of these viruses to stably express high levels of both AhR gene and GFP marker gene in cultured cells and in mice mammary glands.
- Successfully establishing for the first time, a method for *in situ* viral infection to mouse mammary glands, as a means of introducing genes in a mammary gland.
- Design and synthesis of four siRNA for human AhR
- Development and banking of AhR-KO mouse embryo fibroblasts.
- Abstract-poster was presented at the 96th AACR meeting (Appendix 1).
- Abstract-poster was presented at the Era of Hope Department of Defense Breast Cancer Research Program meeting (Appendix 2)
- Two manuscripts are published form work related to this project and was running parallel to this project (appendix 7 &8)
- A manuscript is submitted and provisionally accepted (Appendix 9).
- A manuscript is in preparation to be submitted.
- Two dissertations were submitted to the graduate school at Meharry Medical College in partial fulfillment of the requirement for doctorate of philosophy (Ph.D.) degrees in Pharmacology (Dr. Joann Brooks 2005, who is currently a FIRST fellowship awardee

Postdoctoral Associate at the Winship Cancer Institute, Emory University, GA; and Dr. Yolanda Dale 2006, who is currently a Sallie Kaplan postdoctoral fellow at the National Cancer Institute, NIH).

- Data from this grant will be used as preliminary data for a research project grant from NIH.

Bibliography of manuscripts and meeting abstracts submitted in connection to this research grant:

1. Brooks J and **Eltom SE**. Overexpression of the aryl hydrocarbon receptor in mammary epithelial cells increases proliferation. Presented at the 96th Annual Meeting of the American Association for Cancer Research, Anaheim CA, April 16-20, 2005.
2. Brooks J and **Eltom SE**. Malignant transformation of mammary epithelial cells by overexpression of the aryl hydrocarbon receptor. Presented at the Era Of Hope, Department of Defense Breast Cancer Research Program Meeting, June 8-11, 2005.
3. Brooks J and **Eltom SE**. Over-expression of the aryl hydrocarbon receptor induces malignant transformation of mammary epithelial cells. Presented at the 45th Annual Meeting of Society of Toxicology, in San Diego, CA, March 5-9, 2006.
4. **Eltom, SE**, Gasmelseed, AA and Saoudi-Guentri D. The aryl hydrocarbon receptor is over-expressed and constitutively activated in advanced breast carcinoma. Presented at the 97th Annual Meeting of the American Association for Cancer Research, Washington, DC, April 1-6, 2006.
5. Dale YR and **Eltom SE**. Calpain mediates the dioxin-induced activation and down-regulation of the aryl hydrocarbon receptor in metastatic breast cancer cell lines. Presented at the 97th Annual Meeting of the American Association for Cancer Research, Washington, DC, April 1-6, 2006.
6. Dale YR and **Eltom S.E** (2006). The induction of CYP1A1 by Oltipraz is mediated through calcium-dependent-calpain. *Toxicol. Letters* **166**:150-159.
7. Dale YR and **Eltom SE** (2006) Calpain mediates the dioxin-induced activation and down-regulation of the aryl hydrocarbon receptor. *Mol. Pharmacol.* **70**: 1481-1487.
8. Brooks JA and **Eltom S.E.** (2006) Over-expression of the aryl hydrocarbon receptor induces malignant transformation of mammary epithelial cells. *Provisionally Accepted, Breast Cancer Research*
9. **Eltom, S.E**, C.R. Jefcoate, A.A. Gasmelseed and D. Saoudi-Guentri. The aryl hydrocarbon receptor is over-expressed and constitutively activated in advanced breast carcinoma Cell lines. *In preparation to be submitted to Cancer Research.*

Personnel received pay from the grant:

1. Sakina Eltom, DVM, PhD- Principal Investigator, June 2002-June 2005.
2. Jaikun Wang, MD, PhD- Postdoctoral Associate, February 2002-June 2004
3. Dajla Saoudi-Guentri, MD- Postdoctoral Associate, July 2004-June 2005

Conclusions

A role for AhR in breast cancer initiation and promotion is becoming more definitive. In this study we have shown that AhR alone is capable of transforming immortalized normal mammary epithelial cells into a malignant phenotype. The results of the addressed aims that help to prove our hypothesis are: (1) We have shown that AhR over-expression leads to increased AhR activity upon activation as well as constitutive activation in the absence of agonist stimulation. The constitutive expression of CYP1A1 seen by over-expressing AhR is an observation seen also in metastatic breast cancer cells, which exhibit high AHR expression. In both the H16-overexpressing AhR cells and the metastatic MT2, this constitutive expression is a product of AhR being localized in the nucleus. (2) We have also shown that increase in AhR expression in the normal mammary epithelial cells also increases their proliferation to a rate comparable to the metastatic cell line. This is also reflected in an increase of cells transitioning through the cell cycle. An increased rate of transition out of G0/G1 may not provide the cells with the appropriate amount of time necessary to prevent DNA mutations from entering the synthesis phase. This is another possible mechanism by which increases in AhR expression may lead to carcinogenesis. In addition, we have been able to show that increases in AhR expression can lead to the ability of a cell to gain invasive potential. Invasiveness is an essential characteristic of transformed cells and certainly defines a cell as malignant.

Our results indicate that AhR is capable of transforming normal mammary epithelial cells. However, some of the data derived in this study does not support the notion that AhR is responsible for the malignant state of the metastatic mammary epithelial cells. However, the inability of decreased AhR expressions to revert the metastatic phenotype to a more normal phenotype may be a consequence of increasing mutations. Cancer cells readily acquire defects in the repair process that accelerate the mutation rate and genetic instability is a consequence of defective repair mechanisms. It is feasible to speculate that even if AhR is capable of inducing

transformation in normal mammary epithelial cells, increased mutations following the initial event may be too extensive to reverse that transformation by merely removing the causative agent. A large advantage to this study is the acquisition of both the normal and metastatic cell lines being derived from a single individual. This eliminates biological variations between cell lines and more definitely implicates AhR as the causative factor in the transformation observed. An obvious step in determining the mechanism behind AhR ability to transform the normal mammary epithelial cells is to determine what other proteins are affected by the increase in AhR expression. Several pathways proven to play an important role in carcinogenesis have already been implicated in interacting with the AhR pathway. Determining whether the expression of genes within these implicated pathways is regulated by AhR would be a major step toward understanding the mechanism by which AhR contributes to carcinogenesis. Microarray analyses of differential gene expression are underway as the next step to investigate these pathways, which are directly regulated by AhR.

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session at the 50th Annual Symposium on Fundamental Cancer Research: Molecular Determinants of Cancer Metastasis. October 28-31, 1997. Houston, Texas.

Appendices

- Appendix 1: Abstract presented at the 96th Annual Meeting of the American Association for Cancer Research (2005)- 1 page.
- Appendix 2: Abstract presented at the Era Of Hope, Department of Defense Breast Cancer Research Program Meeting (2005)- 1 page.
- Appendix 3: Abstract presented at the 45th Annual Meeting of Society of Toxicology (2006)-1 page.
- Appendix 4: Abstract presented at the 97th Annual Meeting of the American Association for Cancer Research (2006)-1 page.
- Appendix 5: Manuscript published in Molecular Pharmacology (7 pages)
- Appendix 6: Manuscript published in Toxicology Letters (10 pages)
- Appendix 7: Manuscript provisionally accepted in Breast Cancer Research (35 pages).

Cellular and Molecular Biology 67: Cell Cycle Control and Cancer 3

Abstract #5429

Overexpression of the aryl hydrocarbon receptor in mammary epithelia cells increases proliferation

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There is a growing interest surrounding role the Aryl hydrocarbon receptor (AhR) in carcinogenesis; however, little is known about the mechanism by which AhR may exert its carcinogenic effect. AhR is a cytosolic basic helix-loop-helix (bHLH) protein that upon activation by polyaromatic hydrocarbons (PAH), translocates to the nucleus and heterodimerizes with another bHLH, the aryl hydrocarbon nuclear translocator (ARNT) to increase transcription of certain genes including CYP1A1 and CYP1B1. Biochemical and molecular biology studies have revealed that the AhR mediates the toxic and biological effects of environmentally persistent PAHs, the most potent of which is 2,3,7,8-tetrachloro-dibenzo-p-dioxin (TCDD). Activation of AhR by TCDD in cultured cell lines has been shown to cause a block in G1 to S-phase cell cycle transition. Also, several lines of evidence suggest that AhR is involved in regulating cell proliferation. Experiments were designed to address the question of whether AhR over-expression alone is sufficient to increase proliferation and alter cell cycle distribution. High levels of the AhR were expressed in immortalized normal mammary epithelial cells by stably transfecting human AhR cDNA using retroviral gene expression vectors. The level of AhR protein was determined by immunoblotting. The generate clones over-expressing AhR were shown to have a significant increase in the rate of proliferation. Cells over-expressing AhR showed a 95% increase in proliferation over normal cells during a 24h period. Also fluorescence activated cell sorting (FACS) analysis demonstrated that the increased levels of AhR result in a decrease in the percent of cells remaining in G0/G1. Normal cells contained 76% of cells in G0/G, while cells over-expressing AhR resulted in 36% remaining in G0/G1. However the decrease in G0/G1 is reflected by an increase in both S-phase and G2/M distribution. Together, this data suggest a mechanism by which AhR can enhance mutations by decreasing the time allotted for checkpoints thus leading to increase carcinogenesis.

P29-4: OVEREXPRESSION OF THE ARYL HYDROCARBON RECEPTOR IN MAMMARY EPITHELIAL CELLS INCREASES PROLIFERATION BY INCREASING G1/S PHASE TRANSITION

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There is a growing interest surrounding role the Aryl hydrocarbon receptor (AhR) in exerting the carcinogenic effect of polycyclic aromatic hydrocarbons (PAHs); however, little is known about the mechanism by which AhR may exert its carcinogenic effect. AhR is a cytosolic basic helix-loop-helix (bHLH) protein that upon activation by PAHs, translocates to the nucleus and heterodimerizes with another bHLH, the aryl hydrocarbon nuclear translocator (ARNT) to increase transcription of certain genes including CYP1A1 and CYP1B1. Biochemical and molecular biology studies have revealed that the AhR mediates the toxic and biological effects of environmentally persistent PAHs, the most potent of which is 2,3,7,8-tetrachloro-dibenzo-p-dioxin (TCDD). Activation of AhR by TCDD in cultured cell lines has been shown to cause a block in G1 to S-phase cell cycle transition. Also, several lines of evidence suggest that AhR is involved in regulating cell proliferation. Experiments were designed to address the question of whether AhR over-expression alone is sufficient to increase proliferation and alter cell cycle distribution. High levels of the AhR were expressed in immortalized normal mammary epithelial cells by stably transfecting human AhR cDNA using retroviral gene expression vectors. The level of AhR protein was determined by immunoblotting. The generated clones over-expressing AhR were shown to have a significant increase in the rate of proliferation. Cells over-expressing AhR showed a 3-fold increase in proliferation over normal cells during a 24h period. Also fluorescence activated cell sorting (FACS) analysis demonstrated that the increased levels of AhR result in a decrease in the percent of cells remaining in G0/G1. Normal cells contained 76% of cells in G0/G1, while cells over-expressing AhR resulted in 36% remaining in G0/G1. However the decrease in G0/G1 is reflected by an increase in both S-phase and G2/M distribution. Together, this data suggest a mechanism by which AhR can contribute to carcinogenesis.

The U.S. Army Medical Research and Materiel Command under DAMD17-03-1-0458 and DAMD17-02-1-0483 supported this work.

treated AhR null: 26 ± 1.3 nmol/ml, $p < 0.050$), a non-specific assessment of ROS production. Further, BQ-123 reduced both cardiac lucigenin chemiluminescence (AhR null: 7.3 ± 0.4 ; BQ-123-treated AhR null: 4.1 ± 0.2 ; AhR wildtype: 3.7 ± 0.2 RLU/mg tissue/5 min, $p < 0.001$) and cardiac mRNA expression of NAD(P)H oxidase subunits gp91phox, p47phox, and p67phox, in AhR null mice, compared to wildtype. These findings demonstrate that ET-1 activation of ET_A receptors mediates an increase in ROS which is associated with cardiac hypertrophy in AhR null mice. Further, the ET-1-mediated increase in ROS appears to be a result of increased NAD(P)H oxidase activation in AhR null mice. Supported by ES010433 to MKW; P30 ES12072 to UNM.

356 CHARACTERIZATION OF HSP90-BINDING TO THE AH RECEPTOR, CENTRAL ROLE OF THE PASB DOMAIN

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The Ah receptor (AhR) is a ligand-dependent transcription factor, which regulates the biochemical and toxic effects of structurally diverse chemicals. Hsp90, one subunit of the AhR complex, appears to direct proper folding and maintenance of the high affinity ligand binding conformation of the AhR in some species. Using a structural homology model we developed for the ligand- and hsp90-binding PASB domain of the AhR to guide our mutagenesis, we have examined the physical interactions of hsp90 with the AhR and subsequent effects on AhR functionality (hsp90, ligand and DNA binding and transcriptional activation). Deletion of the PASB domain resulted in the complete loss of hsp90-binding and constitutive ligand-independent activation of DNA-binding and reporter gene transcription, suggesting that documented interactions of hsp90 with the AhR bHLH domain are insufficient on their own for hsp90 binding. Swapping of the PASB domain of Arnt (which does not bind hsp90) for that of the AhR did not completely eliminate hsp90 binding suggesting that the Arnt PASB domain can confer and/or maintain weak hsp90 binding in the context of the full-length AhR; binding through the bHLH site is dependent on the presence of the intact PASB domain. Deletions within the AhR PASB domain resulted in intermediate levels of hsp90 binding and revealed that the bulk of the central PASB 5 strand b-sheet is required for the optimal hsp90-binding. PASB deletions excluding amino acids 339-362 resulted in ligand-independent transformation and DNA-binding, similar to full PASB deletion. Based on the AhR PASB model, these results not only indicate that two b-strands with the connecting flexible loop are essential for ligand-induced activation of AhR transformation, but they suggest that ligand binding to the PASB domain may induce a conformational change in this region that weakens its association with hsp90 exposing the AhR bHLH-PASA dimerization domain for Arnt. (NIH ES07685).

357 THE ROLE OF ENDOGENOUS XAP2 IN THE SUBCELLULAR LOCATION AND NUCLEOCYTOPLASMIC SHUTTLING OF THE ENDOGENOUS Ah^{b-1} RECEPTOR

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The endogenous Ah^{b-1} receptor expressed in the murine Hepa-1 cell line is primarily localized to the cytoplasm and does not accumulate in the nucleus when nuclear export is blocked by leptomycin B (LMB). Studies using transient expression systems have implicated the immunophilin-like XAP2 protein in the control of the localization of the Ah^{b-1} receptor and suggest that XAP2 dissociates prior to ligand-mediated nuclear localization. To evaluate the role of endogenous XAP2 on the localization of the endogenous Ah^{b-1} receptor, Hepa-1 cells were exposed to TCDD for 0, 15, 30, 45 and 60 minutes and harvested for immunoprecipitation studies (IP) or fixed and immunostained. TCDD exposure resulted in the translocation of the AHR to the nucleus within 30 minutes, yet equal amounts of XAP2 were precipitated with the AHR at all time points. XAP2 was also detected in association with the non-degraded AHR fraction that remained in the cells following 4 hours of TCDD exposure. Reduction of endogenous XAP2 in Hepa-1 cells with siRNA, resulted in an Ah^{b-1} receptor that was not associated with significant levels of XAP2, yet retained a cytoplasmic localization in the absence of ligand. However, in these cells, the endogenous Ah^{b-1} receptor could be detected in the nucleus following exposure to LMB. Truncation of the COOH-terminal 305 amino acids of the Ah^{b-1} receptor resulted in an AHR protein that exhibited a predominant nuclear localization and was associated with the same level of XAP2 as full-length AHRs that exhibited a cytoplasmic localization. These studies support a role of the XAP2 protein in the cytoplasmic retention of the unliganded full-length Ah^{b-1} receptor. However, in the absence of the COOH-terminal domain, XAP2 remains associated with the AHR but does not function to retain the receptor in the cytoplasm. In addition, the studies indicate that XAP2 does not dissociate from the endogenous Ah^{b-1} receptor following ligand binding. Supported by NIH grant ES10991 (RSP).

358 3-METHYLCHOLANTHRENE AND OTHER ARYL HYDROCARBON RECEPTOR AGONISTS DIRECTLY ACTIVATE ESTROGEN RECEPTOR ALPHA

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3-Methylcholanthrene (3MC) is an aryl hydrocarbon receptor (AhR) agonist, and it has been reported that 3MC induces estrogenic activity through AhR-estrogen receptor α (ER α) interactions. In this study, we used 3MC and 3,3',4,4'-pentachlorobiphenyl (PCB) as prototypical AhR ligands, and both compounds activated estrogen-responsive reporter genes/gene products (cathepsin D) in MCF-7 breast cancer cells. The estrogenic responses induced by these AhR ligands were inhibited by the antiestrogen ICI 182780 and by transfection of a small inhibitory RNA (siRNA) for ER but were not affected by an siRNA for AhR. These results suggest that 3MC and PCB directly activate ER α , and this was confirmed in a competitive ER α binding assay and in a fluorescence resonance energy transfer (FRET) experiment where PCB and 3MC induced CFP-ER α /YFP-ER α interactions. In a chromatin immunoprecipitation assay, PCB and 3MC enhanced ER α (but not AhR) association with the estrogen responsive region of the pS2 gene promoter. Moreover, in AhR knockout mice, 3MC increased uterine weights and induced expression of cyclin D1 mRNA levels. These results demonstrate that PCB and 3MC directly activate ER α -dependent transactivation and extend the number of ligands that activate both AhR and ER α .

359 MALIGNANT TRANSFORMATION OF MAMMARY EPITHELIAL CELLS BY OVER-EXPRESSION OF THE ARYL HYDROCARBON RECEPTOR

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The aryl hydrocarbon (Ah) receptor, which is well known for its mediation of the toxic responses to the environmental poly-halogenated aromatic hydrocarbons (PAH), is a ligand activated basic helix-loop-helix transcription factor. Many reports have documented the role of the Ah receptor (AhR) in PAH-induced carcinogenicity, however in this report we addressed whether the over-expression of the AhR alone is sufficient to induce carcinogenic transformation in mammary epithelial cells. Retroviral expression vectors were used to stably express high levels of AhR proteins in an immortalized normal human mammary epithelial cell line (HMEC) with low background AhR expression. Series of HMEC stables with varying expression levels of AhR were generated. Clones overexpressing AhR by more than 3-fold showed a two fold decrease in the population doubling time compared to vector-control cells. Cell cycle analysis revealed that this enhancement in proliferation rate was mainly due to an increase in the percentage of cells transiting from G0/G1 to S- and G2/M phases. The overexpression of AhR has resulted in morphological transformation of these HMEC into a fibroblast-like cells with acquired enhanced motility and increased in their migration by more than two folds compared to their vector-expressing clones. Most significantly, these transformed cells have acquired the ability to invade matrigel matrix, where more than 80% of plated cells invaded the matrix and crossed the membranes within 24 h. In contrast, none of the vector controls or the parent HMEC were able to invade matrigel. Furthermore, these malignant phenotypes were coupled with the ability of the clones to form colonies in soft agar, reflecting their malignant transformation. Collectively, these data provide the first evidence for the direct role of AhR in progression of breast carcinoma. Funded by G12-RR03032, U54-CA91408-03, DAMD17-02-1-0483, DAMD17-02-01-0458.

360 THE DIFFERENTIAL RECRUITMENT OF ER α TO CYP1A1 BY BNF, ICZ, AND DIM AND THE IMPORTANT ROLE OF ER α IN AHR TRANSCRIPTION

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We have recently described the TCDD-dependent recruitment of estrogen receptor alpha (ER α) to AhR regulated target genes CYP1A1 and CYP1B1. However, whether and to what extent other AhR agonists induce the recruitment of ER α to CYP1A1 is not known. Using ChIP assays in T47D breast cancer cell line, we demonstrate that beta naphthoflavone (BNF), diindolylmethane (DIM) and indolo[3,2-b]carbazole (ICZ) induce the recruitment of ER α to CYP1A1, although the level of promoter occupancy of ER α varied among the different ligands. BNF, TCDD and ICZ induced a 10-fold promoter enrichment of ER α to CYP1A1 compared to solvent controls, whereas DIM induced an 80-fold enrichment.

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Abstract #1730

The aryl hydrocarbon receptor is over-expressed and constitutively activated in advanced breast carcinoma

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The aryl hydrocarbon receptor (AhR), a ligand-activated helix loop helix transcription factor, binds environmental poly aromatic hydrocarbons (PAH) such as dioxin, and mediates their toxicity, including carcinogenesis. This study was designed to investigate the functional significance of AhR in breast carcinogenesis. The AhR expression and its transcriptional activity was analyzed in a battery of human breast carcinoma (HBC) cell lines with varying degrees of malignancy in comparison to immortalized normal and primary human mammary epithelial cells (HMEC). Western immuno-blotting revealed dramatic elevated levels of AhR proteins in tumorigenic HBC of advanced malignancy (MD231, MDA468, ZR-75, MDA435, MCF-7), while less levels were expressed in HBC typically categorized as early stages of malignancy (T-47D, HBL100, BT-549), normal immortalized (H16N2 and MCF10A) and primary HMEC. RT-PCR analysis of mRNA revealed a similar trend although not as dramatic high levels, suggesting a role for protein stabilization in these elevated levels. These results were further confirmed in Sager's 21T series, which are closely matched pairs of HBC derived from a single patient and are characterized by exhibiting a gradient order of malignancy (21MT2>21NT>21PT). The 21MT-2 lines showed the highest expression of protein and mRNA and 21NT was medium between 21MT-2 and 21PT lines. This high expression of AhR is independent of estrogen receptor (ER) status, as verified in MDA 231 (ER negative) and its variant S30 (ER positive), as well as T47D-A18 (ER positive) and its variant T47D-C4:2W (ER negative), as well as in 21T series which are all ER negative. The AhR is usually localized in the cytoplasm of most normal cells including HMEC and is translocated to the nucleus upon ligand (dioxin) activation. However, both sub-cellular fractionation experiments and fluorescence immuno-cytochemical staining has shown that the AhR in the HBC are predominantly localized to the nuclear compartments in absence of ligand treatment. Similarly, immuno-histochemical analysis of human breast tumors has shown an increase in AhR expression in the invasive carcinomas, where the AhR staining was predominantly or exclusively nuclear. Notably, this nuclear accumulation of AhR in untreated HBC was transcriptionally active as evidenced by the substantial expression of CYP1A1 mRNA, which is exclusively regulated transcriptionally by the activated AhR. In conclusion, this study reports a novel finding of elevated levels of AhR in human breast carcinomas in direct proportion to their degree of malignancy. These data identify the AhR as a possible regulator of breast cancer progression and its possible consideration as a candidate prognostic factor for survival as well as its potential as a target for breast cancer therapeutic intervention.

ACCELERATED COMMUNICATION

Calpain Mediates the Dioxin-Induced Activation and Down-Regulation of the Aryl Hydrocarbon Receptor

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ABSTRACT

The aryl hydrocarbon receptor (AhR) is a ligand-activated basic-helix-loop-helix transcription factor that binds polycyclic aromatic hydrocarbons (PAH), such as 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD), and mediates their toxicity. Binding of PAH to AhR in the cytoplasm triggers a poorly defined transformation step of the receptor into a nuclear transcription factor. In this study, we show that the calcium-dependent cysteine protease calpain plays a major role in the ligand-induced transformation and signaling of AhR. Fluorescence imaging measurements showed that TCDD treatment elevates intracellular calcium, providing the trigger for calpain activation, as measured toward *t*-butoxycarbonyl-Leu-Met-chloromethylaminocoumarin, a calpain-specific substrate. Inhibition of calpain activity by the *N*-benzyloxycarbonyl-Val-Phe-aldehyde (MDL28170) blocked the TCDD-induced nuclear translocation of AhR in Hepa1c1c7

mouse hepatoma cell line. Treatment of the human metastatic breast carcinoma cell line MT-2 with MDL28170 and 3-(4-iodophenyl)-2-mercapto-(*Z*)-2-propenoic acid (PD 150606), two calpain-selective inhibitors, completely abolished the TCDD-induced transactivation of AhR as assessed by transcription of *CYP1A1* gene. Previous studies have established that after TCDD-induced transactivation, the AhR undergoes a massive depletion; we show here that selective calpain inhibitors can block this step, which suggests that the ligand-induced down-regulation of the AhR is calpain-dependent. The data presented support a major role for calpain in the AhR transformation, transactivation, and subsequent down-regulation, and provide a possible explanation for many of the reported phenomena of ligand-independent activation of AhR.

The AhR is a ligand-activated basic helix-loop-helix transcription factor that regulates the adaptive and toxic responses to a variety of environmental carcinogens, including polycyclic aromatic hydrocarbons (PAH), such as TCDD (Poland and Knutson, 1982). In the absence of ligand, the AhR resides predominantly in the cytoplasm in a conformation stabilized by chaperone proteins hsp90, XAP2, and p23 (Carver and Bradfield, 1997; Ma and Whitlock, 1997; Meyer and Perdew,

1999). The current working model for the AhR signaling proposes that ligand binding to AhR facilitates the dissociation of the chaperone proteins and AhR transformation into a form that readily translocates to the nucleus. In the nucleus, AhR dimerizes with the related bHLH aryl hydrocarbon receptor nuclear translocator (ARNT) protein (Kazlauskas et al., 2001), and binding of this heterodimer to DNA recognition motifs designated as xenobiotic-responsive elements results in enhanced transcription of the Ah-responsive genes (Jones et al., 1985), typified by *CYP1A1* and *CYP1A2* (Gonzalez et al., 1984). The protein products of these cytochrome P450 genes are catalytically active in metabolizing not only many endogenous compounds such as β -estradiol, but also many drugs, dietary components, mutagens, carcinogens,

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ABBREVIATIONS: AhR, aryl hydrocarbon receptor; PAH, polycyclic aromatic hydrocarbons; hsp90, 90-kDa heat shock protein; ARNT, aryl hydrocarbon receptor nuclear translocator; MDL 28170, *N*-benzyloxycarbonyl-Val-Phe-aldehyde; PD 150606, 3-(4-iodophenyl)-2-mercapto-(*Z*)-2-propenoic acid; MG-132, *N*-benzyloxycarbonyl (*Z*)-Leu-Leu-leucinal; TCDD, 2,3,7,8-tetrachlorodibenzo-*p*-dioxin; BOC-LM-CMAC, *t*-butoxycarbonyl-Leu-Met-chloromethylaminocoumarin; AM, acetoxymethyl; PCR, polymerase chain reaction; DMSO, dimethyl sulfoxide; TBST, Tris-buffered saline-Tween 20.

and environmental pollutants (Conney, 1982). After transcriptional activation, the liganded-AhR undergoes a rapid degradation (Prokipcak and Okey, 1991; Reick et al., 1994; Pollenz, 1996). Studies have suggested that this ligand-induced down-regulation of AhR is proteasome-dependent (Davarinos and Pollenz, 1999) and that the nuclear export is required for this process (Song and Pollenz, 2002).

Although forced dissociation of the chaperone proteins, especially hsp90 by geldanamycin, allows for the nuclear translocation of the receptor, it is not sufficient for its transactivation (Song and Pollenz, 2002). In vitro studies have shown the AhR to be a substrate for calpain (Poland and Glover, 1988), a member of a family of cytosolic calcium-dependent cysteine proteases. Calpain is involved in regulating many cellular processes, including proliferation, differentiation, cell motility, and metastasis through regulation of signal transduction and cleavage of many target cellular regulatory proteins (Wang, 1990; Potter et al., 1998). Of the several calpain isoforms, calpain I (μ -calpain), and calpain II (m-calpain) are ubiquitous enzymes, activated with low and high calcium concentrations, respectively. Because the treatment of cells with PAH can elicit a rapid increase in intracellular calcium (Hanneman et al., 1996; Tannheimer et al., 1997), we hypothesize that this increase in intracellular calcium could provide the trigger to activate calpain. In this study, we have examined the involvement of calpain in the transformation process required for the nuclear translocation, transactivation, and subsequent degradation of AhR.

Materials and Methods

Materials. Calpain inhibitor III (MDL 28170), PD 150606, MG-132, epoxomicin, and ionomycin were purchased from Calbiochem (San Diego, CA). Dioxin (TCDD) was purchased through NCI Chemical Carcinogen Repository—Midwest Research Institute (Kansas City, MO). The calpain substrate BOC-LM-CMAC and Fluo-4-AM were purchased from Invitrogen (Carlsbad, CA). Real-time PCR kit was purchased from Bio-Rad Laboratories (Hercules, CA). The rabbit polyclonal anti-AhR antibodies (Poland and Glover, 1990; Pollenz et al., 1994) were a kind gift from Dr. Christopher Bradfield (University of Wisconsin, Madison, WI). The Sager MT-2 metastatic cell line was derived from a patient with an infiltrating intraductal carcinoma and was kindly provided by Dr. Vilma Band (Northwestern University, Chicago, IL).

Cell Culture and Stimulation of MT-2 Cells. The metastatic MT-2 cell line was grown in DFCI-1 medium as described previously (Band et al., 1990). For experiments, MT-2 cells were seeded in six-well plates at a density of 5×10^5 cells per plate and grown for 24 h. Cells were preincubated with inhibitors MG-132, epoxomicin, or MDL 28170 for 2 h and maintained during 3-h TCDD treatment. TCDD, MG-132, MDL 28170, and epoxomicin were solubilized in DMSO, with an equivalent volume added to control cells [maximum of 0.1% (v/v)].

Intracellular Calcium Measurements. MT-2 cells cultured in 24-well plates (2×10^4) in DFCI-1 medium were loaded with $5 \mu\text{M}$ Ca^{2+} -sensitive dye Fluo-4-AM (Invitrogen) for 45 min at 37°C . After preincubation, cells were rinsed three times with DFCI medium to remove free dye and continued to incubate for 30 min in medium alone to allow complete de-esterification of AM esters. Fluo-4-loaded cells were then stimulated with 1 or 10 nM TCDD, 10 μM ionomycin, or vehicle alone for 25 min. Changes in intracellular calcium were measured as captured fluorescence images of cells using a fluorescence microscope (excitation at 385 nm, emission at 512 nm; IX50; Olympus, Tokyo, Japan).

Calpain Activity Assay. Calpain activity in MT-2 cells was assessed by fluorescence microscopy using the calpain substrate BOC-LM-CMAC (Invitrogen). The nonfluorescent cell-permeable substrate is conjugated by intracellular thiols into a membrane impermeable form, allowing substrate accumulation within the cell (Carragher et al., 2004). Proteolytic cleavage of BOC-LM-CMAC by calpain results in blue fluorescence. Cells in 24-well plates were pretreated with 15 μM calpain inhibitor MDL28170, MG-132, or epoxomicin followed by TCDD or ionomycin treatment. In brief, cells were incubated with 50 μM BOC-LM-CMAC for 20 min at 37°C . Fluorescence intensity corresponding to calpain activity was visualized, and images were captured with an Olympus IX50 fluorescence microscope using a digital camera with MagnaFire software, and quantified by ImageJ software (<http://rsb.info.nih.gov/ij/>). The image exposure settings were identical within each experiment. Data for each experiment were normalized to ionomycin values (set as 100%).

Immunocytochemical Staining and Fluorescence Microscopy. Cells growing on cover slips in six-well plates were washed in phosphate-buffered saline and then fixed by incubation in a (1:1) methanol/acetone solution at 4°C for 30 min and subsequently air-dried. For staining, cells were rinsed and hydrated with TBST (10 mM Tris-HCl, 150 mM NaCl, and 0.05% Tween 20) and transferred to clean six-well plates. The cover slips were incubated at room temperature for 1 h in 4% milk solution in TBST to block nonspecific binding. The cover slips were then incubated at room temperature for 1 h in 1 $\mu\text{g}/\text{ml}$ anti-AhR polyclonal antibody (BEAR-4) in 2% milk solution in TBST while rocking. Cover slips were then washed three times (15 min each) with TBST. A 1:200 dilution of fluorescein isothiocyanate-conjugated goat anti-rabbit antibodies in 2% milk with TBST was added to the cover slips in reduced light and incubated at room temperature for 1 h. The cover slips were then washed extensively and mounted onto glass slides using mounting solution containing 1,4-diazabicyclo[2.2.2]octane as an anti-fading agent.

Preparation of Total Cell Lysates and Immunoblotting. After treatments, cell monolayers were lysed in 1 ml of TRIzol, which allowed for simultaneous isolation of RNA and protein. After lysis, both RNA and protein were isolated according to the vendor's instructions. The protein pellets were resuspended in 2% SDS and sonicated briefly to dissolve. The protein concentration in cell extracts was determined using a BCA assay kit, per the manufacturer's instructions. Equivalent amounts of protein (10 μg) were separated by SDS polyacrylamide gel electrophoresis and transferred for 2 h at 175 V to polyvinylidene difluoride membranes. The membranes were blocked at room temperature for 1 h in 4% nonfat milk in TBST with subsequent incubation with BEAR-3 anti-AhR (1 $\mu\text{g}/\text{ml}$). After brief washing, blots were incubated with the corresponding horseradish peroxidase-coupled anti-rabbit or anti-mouse secondary antibody (1:20,000) for 1 h followed by additional washing in TBST and TBS. Reactive protein bands were visualized using enhanced chemiluminescence reagents. Band density was quantified by UVP Bio-Imaging System using LabWorks Image Acquisition Analysis Software (UVP Inc., Upland, CA). Thereafter, blots were probed with actin monoclonal antibodies (1:4000) for normalization of protein loading. The relative levels of AhR protein were then normalized to the level of β -actin to generate normalized values for the relative concentration of AhR in each sample.

Reverse Transcriptase Polymerase Chain Reaction. After lysis with TRIzol, total RNA was isolated according to manufacturer's protocol. cDNA was prepared from 2 μg of mRNA using random hexamer primers and Moloney murine leukemia virus reverse transcriptase. CYP1A1 PCR amplification was done using forward primer sequence 5'-TAG ACA CTG ATC TGG CTG CAG-3' and the reverse primer sequence 5'-GGG AAG GCT CCA TCA GCA TC-3'. Housekeeping gene glyceraldehyde 3-phosphate dehydrogenase was amplified as an internal control using forward primer 5'-ACC ACA GTC CAT GCC ATC AC-3' and reverse primer 5'-TCC ACC ACC CTG TTG CTG TA-3'. PCR products were visualized in agarose gels

stained with ethidium bromide, and bands were quantified by densitometric scanning, as described previously (Eltom et al., 1999).

Real Time RT-PCR. Real-time quantitative PCR was performed using an iCycler iQ real-time PCR detection system (Bio-Rad Laboratories). cDNA generated from TCDD-treated MT-2 cells was serially diluted to establish a standard curve (20,000–0.2 pg). Reactions were performed in triplicates using 2.5 μ l of cDNA per 25- μ l reaction containing iQ SYBR green super mix and CYP1A1 primers (5'-CTA TGA CCA CAA CCA CCA AGA ACT G-3' forward primer and 5'-AGG TAG CGA AGA ATA GGG ATG AAC TC-3' reverse primer) with the following PCR parameters: 95°C for 5 min followed by 45 cycles at 95°C for 15 s, 60°C for 30 s, and 72°C for 15 s. Reactions for detection of the endogenous control gene, ribosomal 18S rRNA, were run in parallel for each cDNA template as a reference for normalization using the following primers: 5'-CGG ACA GGA TTG ACA GAT TGA TAG C-3' 18S forward primer and 5'-TGC CAG AGT CTC GTT CGT TAT CG-3' 18S reverse primer. A melting curve analysis was performed for each amplification run to ensure the specificity of product amplification.

Statistical Analysis. The data from different experiments were analyzed using Prism software (GraphPad Software, San Diego, CA) by one-way analysis of variance and Tukey-Kramer multiple comparison tests of values from control versus treated samples

Results

TCDD Mobilizes Calcium in MT-2 Cells. Exposure of human T cells and primary human epithelial cells to PAH leads to the mobilization of intracellular calcium. Because this phenomenon was not observed in the MCF-10A mammary epithelial cell line, which has low concentrations of AhR (Tannheimer et al., 1997), it was important to determine whether TCDD is capable of evoking an increase in intracellular calcium in the MT-2 human metastatic breast cancer cell line, which has high concentrations of AhR. We measured $[Ca^{2+}]_i$ in MT-2 cells in the presence of TCDD, using Fluo-4 AM as a probe. In MT-2 cells, TCDD resulted in an increase in $[Ca^{2+}]_i$ that was comparable with values of the calcium ionophore ionomycin, which results in a profound increase in $[Ca^{2+}]_i$ compared with the solvent control (DMSO) (Fig. 1).

Exposure of Cells to TCDD Activates Calpain. Calpain is activated by elevated intracellular calcium, resulting in auto-proteolytic cleavage to further enhance its activity (Mathiasen et al., 2002). To explore whether TCDD-induced changes in intracellular calcium could lead to calpain activation, whole-cell calpain activity assay was preformed in MT-2 cells using the cell-permeable substrate BOC-LM-CMAC. TCDD exposure resulted in a robust increase in calpain activity, comparable with the levels induced by ionomycin, the ionophore that was used as a positive control (Fig. 2). These data indicate that TCDD could activate calpain. The activation of calpain by TCDD was strongly inhibited by MDL 28170, a potent calpain inhibitor. Figure 2 also shows that MG-132, which has previously been reported to inhibit both proteasomes and calpain (Mathiasen et al., 2002), mimicked the effect of MDL 28170 on TCDD-induced calpain activity. Epoxomicin, which inhibits proteasomes only (Meng et al., 1999), had no effect on calpain activity. These results support the conclusion that TCDD is involved in the activation of calpain in MT-2 cells. The data further establish the selectivity of both MG-132 and MDL 28170 in inhibiting calpain, in agreement with published reports (Potter et al., 1998; Mathiasen et al., 2002).

TCDD-Induced Nuclear Accumulation of AhR Is Calpain-Dependent. To explore whether calpain might be involved in the transformation of AhR leading to its translocation from the cytoplasm into the nucleus, subcellular localization of AhR was analyzed in Hepa-1, the murine hepatoma cell line after treatment with TCDD. Hepa-1 cells were used here because they have no detectable nuclear AhR levels under basal conditions, unlike the human metastatic MT-2 cells, which have substantial nuclear AhR levels in the absence of ligand treatment. TCDD treatment results in enhanced fluorescence nuclear accumulation accompanied by reduction in the cytoplasmic staining, indicative of the receptor nuclear translocation. As shown in Fig. 3, AhR is predominantly localized within the cytoplasm in DMSO-treated control cells, as shown by fluorescence immuno-staining (Fig. 3A). Treatment with MDL 28170 before TCDD exposure resulted in predominant cytoplasmic staining, indicating that calpain influences the localization of the AhR after treatment with TCDD.

Inhibition of Calpain Blocks Transcriptional Activity of AhR. The expression of *CYP1A1*, a gene that is transcriptionally regulated by AhR, is induced by increases in

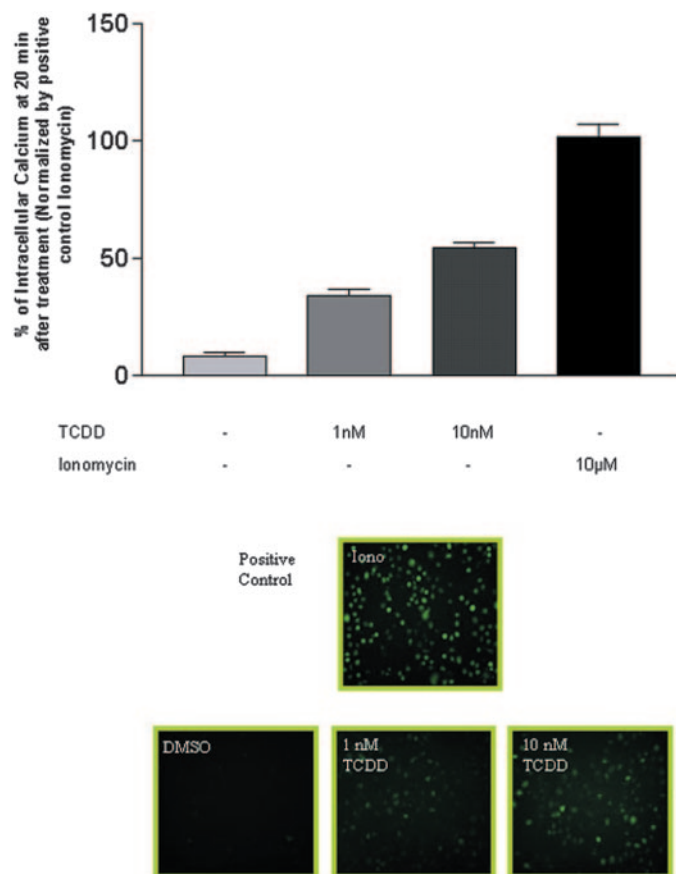


Fig. 1. The effect of TCDD on intracellular free calcium concentration and calpain activation in MT-2 cells. MT-2 cells were preloaded with 5 μ M Fluo-4 AM for 45 min at 37°C. Fluo-4-loaded cells were then stimulated with varying concentrations of TCDD, or 10 μ M ionomycin, and control cells received DMSO for 15 min. Fluorescence images of cells viewed by the IX50 Olympus fluorescence microscope (excitation at 385 nm, emission at 512 nm) were captured by MagnaFire digital camera. Relative fluorescence values for the 20-min time point were quantified using the NIH ImageJ analysis software, and values for each experiment were normalized to ionomycin values; plotted values are average of three independent experiments.

intracellular calcium but the mechanism of this induction is poorly defined (Le Ferrec et al., 2002). It is noteworthy that the disruption of hsp90-AhR complex facilitates nuclear localization of the AhR yet fails to induce gene expression. Based on the data presented in Fig. 3, we presume that calpain-mediated events may be important for AhR-induced transactivation. To this end, we measured *CYP1A1* gene transcription in MT-2 cells treated with MDL 28170 to specifically block the actions of calpain. As shown in Fig. 4A, MT-2 cells have low constitutive levels of *CYP1A1* mRNA, and TCDD treatment resulted in a significant increase in *CYP1A1* mRNA that was suppressed to basal levels by the calpain inhibitors MDL 28170 and PD 150606.

Real-time RT-PCR was also used to provide more quantitative analysis of *CYP1A1* mRNA expression. The results in Fig. 4B show that treatment with TCDD for 3 h resulted in an increase in *CYP1A1* expression of approximately 40-fold over DMSO-treated control. MDL 28170 completely blocked the TCDD ligand-induced *CYP1A1* gene transcription. Likewise, MG-132, which also inhibits calpain, inhibited TCDD-induced *CYP1A1* gene expression to the same degree as MDL28170, whereas epoxomicin, a proteasome inhibitor, had no effect on the TCDD-induced *CYP1A1* expression. Therefore, we conclude that inhibition of calpain preferentially reduces the ability of TCDD to induce the expression of *CYP1A1*.

AhR Degradation after TCDD Treatment. The data presented thus far demonstrate that TCDD mobilizes cal-

cium, triggering calpain activation, which could transform the AhR into a transcription factor, possibly by limited cleavage of the receptor. After enhancing *CYP1A1* transcription, AhR is shuttled from the nucleus to the cytoplasm, where it is degraded. To assess whether calpain contributes to this degradation, TCDD-induced AhR degradation was analyzed in the presence and absence of the calpain inhibitor MDL 28170. Treatment of MT-2 cells with TCDD resulted in greater than 75% reduction in AhR protein levels (Fig. 5A), and pretreatment with MDL 28170 completely blocked this degradation. However, although these treatments with ligand and protease inhibitors had an effect on the AhR levels, they had no effect on the levels of ARNT, the AhR partner for transcriptional activation (Fig. 5A).

Recent reports have implicated proteasomes in the degradation of the AhR; therefore, the proteasome inhibitors MG-132 and epoxomicin were tested. Epoxomicin, a potent and selective proteasome inhibitor, has no cross-activity against nonproteasomal proteases such as calpain (Meng et al., 1999), whereas MG-132 interferes equally with both proteasomes and calpain (Davarinos and Pollenz, 1999; Mailhes et al., 2002). As shown in Fig. 5B, epoxomicin treatment did not protect the receptor from this TCDD-induced down-regulation, whereas MDL 28170 effectively protected the AhR from TCDD-induced down-regulation (Fig. 5B). Unlike epoxomicin, MG-132 inhibited the TCDD-induced degradation of the AhR, to a comparable level of the MDL 28170 (Fig. 5C). These

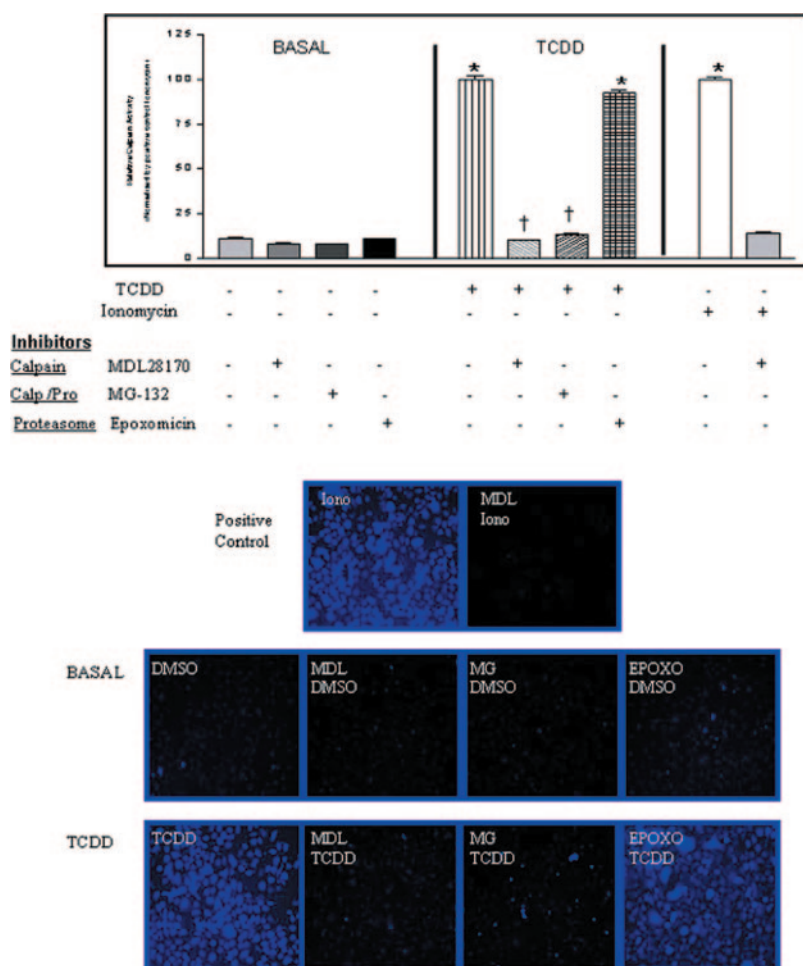


Fig. 2. Activation of calpain in MT-2 cells after exposure to TCDD and ionomycin in the absence and presence of calpain and proteasome inhibitors. Fluorescence intensity corresponding to calpain activity was captured at 20 min by fluorescence microscopy (magnification, 200 \times). Blue fluorescence is indicative of calpain activity. The average fluorescence units of the images were quantified using the ImageJ software from several fields, and plotted values are the average of $n = 3$ independent experiments. *, $p < 0.05$; comparing drug treatments to vehicle control.

results demonstrate that the degradation of the AhR is a calpain-dependent process.

Discussion

PAHs, such as TCDD, elicit a wide range of toxic effects, including carcinogenesis. One way that AhR mediates the toxic responses of these chemicals is through its ability to enhance the transcription of *CYP1A1* gene in many tissues. The protein product of *CYP1A1* catalyzes the bioactivation of these chemicals as well as some endogenous hormones producing reactive metabolites that cause DNA damage and initiate neoplasia. Data presented in this report provide compelling evidence that the Ca^{2+} -dependent protease calpain is a critical player in driving this AhR-mediated process.

For AhR to direct the ligand-induced *CYP1A1* transcription, it has been established that ligand binding to AhR

results in a sequence of events starting with the receptor dissociation from chaperone proteins, such as hsp90, and adoption of conformational changes that allow the AhR to translocate into the nucleus to bind DNA and activate the transcription of *CYP1A1* (Whitlock, 1999). However, the mere dissociation of the hsp90 from the receptor complex, although allowing for AhR nuclear translocation, is insufficient to induce the receptor transactivation (Song and Pollenz, 2002). This observation suggests that additional processing of AhR is required after its dissociation from chaperone proteins. Our data clearly implicate calpain in the transformation required for the AhR nuclear translocation and subsequent transactivation. Inhibition of calpain com-

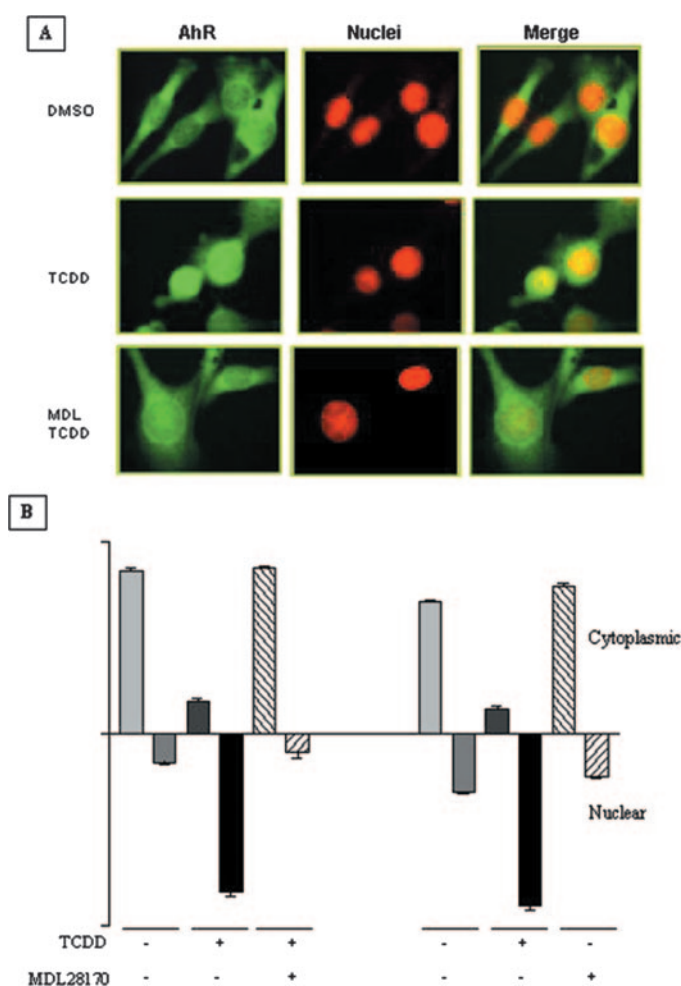


Fig. 3. The effect of calpain on the subcellular localization of AhR in Hepa-1 cells. Murine Hepa cells grown on cover slips were pretreated with calpain inhibitor, MDL 28170 (15 μM), or its vehicle DMSO for 2 h, then exposed for 3 h to 1 nM TCDD or its vehicle DMSO. Cells were fixed and immunostained for AhR followed by fluorescein isothiocyanate-conjugated secondary antibodies as described in the methods. Cells were viewed using the IX50 Olympus Fluorescence microscope and scored for cytoplasmic and nuclear staining from multiple fields. A representative of the cellular staining for AhR is presented in 3A. Cells were scored for cytoplasmic and nuclear staining from multiple fields from the two experiments. Average numbers from two different experiments on the two different cell types (Hepa-1 and MT-2) were normalized to a percentage within each experiment and the average values were plotted in 3B.

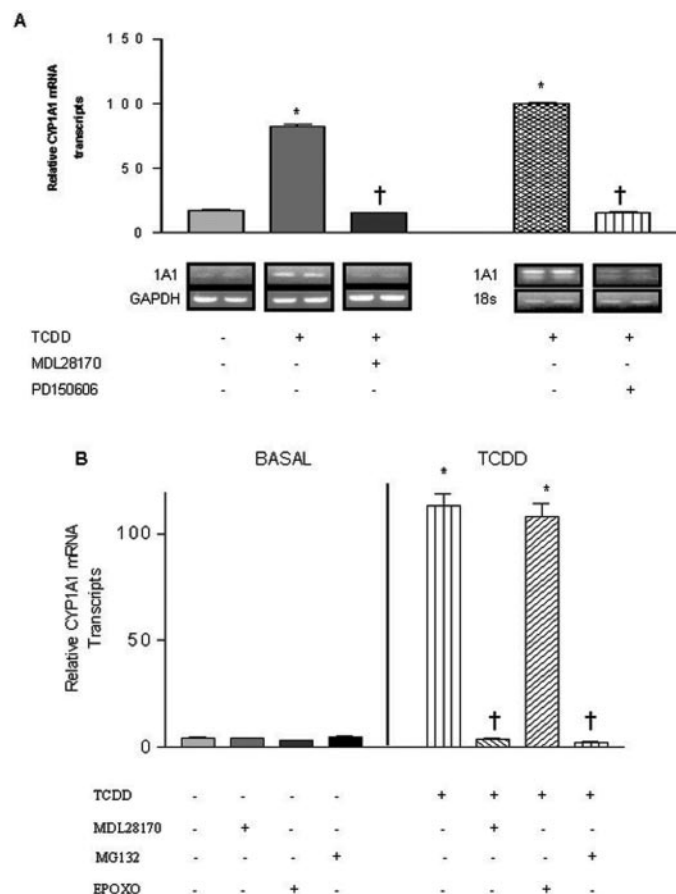
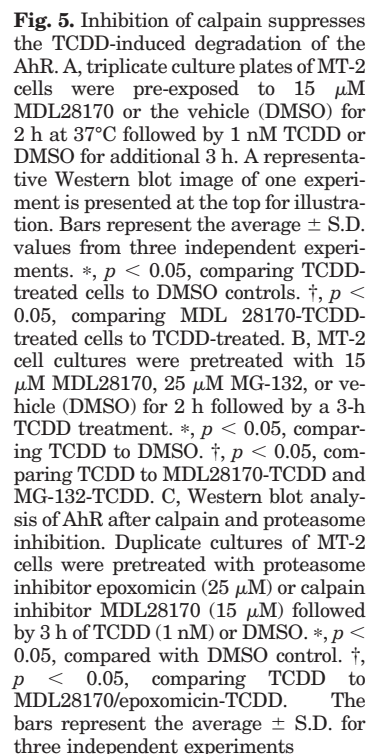


Fig. 4. Inhibition of TCDD-induced *CYP1A1* transcription by treatments that suppress calpain activity. A, RT-PCR analysis of the effect of calpain inhibitors on the TCDD-induced *CYP1A1* expression in MT-2 cells. Cells were pre-exposed to 15 μM PD150606, 15 μM MDL 28170, or their vehicle (DMSO) for 2 h and then treated with TCDD for additional 3 h. The relative expression of *CYP1A1* was quantified as described under *Materials and Methods* and normalized to the level of glyceraldehyde 3-phosphate dehydrogenase or 18S. A representative gel image of one PCR analysis is presented for illustration. The bars represent the average \pm S.D. for three independent experiments and duplicate cultures, which were PCR-assayed in duplicates. *, $p < 0.05$, comparing DMSO- and TCDD-treated cells. †, $p < 0.05$, comparing treatments with TCDD alone to MDL28170/PD150606-TCDD treated cells. B, differential effect of inhibitors of calpain and proteasome on TCDD-induced *CYP1A1* expression. Triplicate cultures of MT-2 cells were pretreated with the different inhibitors or the vehicle for 2 h followed by exposure to TCDD for an additional 3 h. The relative expression of *CYP1A1* mRNA was measured by real-time reverse transcription-PCR and normalized to the levels of 18S mRNA, which was run simultaneously with *CYP1A1* as described under *Materials and Methods*. The bars represent the average \pm S.D. of two independent experiments. *, $p < 0.05$ comparing TCDD to basal levels. †, $p < 0.05$ comparing TCDD to the MDL28170/MG-132-TCDD.



Recent studies have established that AhR, independent of PAH ligands, is directly responsible for inducing cancers of the stomach (Andersson et al., 2002) and pancreas (Koliopanos et al., 2002) and the progression of breast carcinoma (S.E. Eltom, unpublished data). The involvement of calpain in the activation of AhR identifies calpain as a potential therapeutic target for AhR associated cancers. The advantage of this strategy is that calpain exists in a latent form requiring sustained elevation in intracellular calcium.

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The induction of CYP1A1 by oltipraz is mediated through calcium-dependent-calpain

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Abstract

The induction of CYP1A1 expression by oltipraz, a synthetic chemo-preventive agent, which increases intracellular calcium concentration, has previously been shown to result from transcriptional activation of CYP1A1 gene mediated by the Ah receptor (AhR), although oltipraz does not bind the receptor. The present study investigated the possible mechanisms of oltipraz-induced activation of AhR and the subsequent induction of CYP1A1 transcription. Treatment of the human metastatic breast cancer cell line MT-2 with oltipraz results in a concentration-dependent increase in the activity of the calcium-dependent calpain, as measured towards the BOC-LM-CMAC fluorescent substrate. This increase in calpain activity was coupled with the AhR activation, as evidenced by its nuclear localization and increased transcription of CYP1A1 gene. Treatment of cells with calpain specific inhibitor MDL 28170 completely blocked the oltipraz-induced nuclear translocation of AhR and subsequent CYP1A1 expression. Furthermore, treatment with oltipraz resulted in the classical ligand-dependent down-regulation of AhR protein, in a concentration dependent manner. The presented data established for the first time a mechanism of activating AhR and its transcription of CYP1A1 by oltipraz through activation of calcium-dependent calpain.

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Keywords: Ah receptor; CYP1A1; Oltipraz; Intracellular calcium; Calpain

1. Introduction

Cytochrome P450 1A1 (CYP1A1) catalyzes the metabolic activation of polycyclic aromatic hydrocarbons (PAH) resulting in generation of genotoxic metabolites that cause DNA damage and subsequent carcinogenesis (Marston et al., 2001; Shields et al., 1993). CYP1A1 expression is regulated transcription-

ally by PAH through the aryl hydrocarbon receptor (AhR), by a signaling pathway that is well characterized (Denison et al., 1988; Jones et al., 1985). PAH binding to the AhR, which is anchored in the cytoplasm by chaperone proteins hepatitis B virus X-associated protein 2 (XAP2) and heat shock protein (hsp90) (Kazlauskas et al., 2001), leads to the AhR undergoing a transformation step in which the chaperone proteins dissociate. Upon dissociation, the receptor undergoes a conformational change resulting in exposure of the nuclear localization signal (NLS). The NLS is recognized by the α -importin transporter within the nuclear envelope or pore and facilitates nuclear translocation of the AhR (Ikuta et

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al., 1998). Within the nucleus, AhR dimerizes with its partner AhR nuclear translocator (ARNT) and acts as a transcription factor. The dimer then interacts with a 5'-GCGCT-3' DNA sequence, the core binding motif of the xenobiotic-responsive element (XRE), which is present in multiple copies upstream of the CYP1A1 gene promoter (Denison et al., 1988; Jones et al., 1985). Following enhanced gene transcription, the receptor is shuttled from the nucleus into the cytoplasm by chromosome region maintenance protein 1 (CRM-1) export receptor recognition of the nuclear export signal (NES), which is a leucine-rich sequence located within helix 2 domain of the receptor (Davarinos and Pollenz, 1999). Following transcriptional activation, the liganded AhR undergoes a rapid degradation leading to a massive depletion both in vivo and in vitro (Giannone et al., 1998; Harper et al., 1994; Prokipcak and Okey, 1991; Roberts and Whitelaw, 1999). This ligand-dependent down-regulation of AhR have been suggested to be a proteasome-dependent process (Davarinos and Pollenz, 1999; Ma and Baldwin, 2000).

Oltipraz is a synthetic derivative of 1,2-dithiole-3-thione, a constituent of cruciferous vegetables, and it is being developed as a chemopreventive agent (Boone et al., 1990; Liu et al., 1988; Rao et al., 1993; Kensler et al., 1987; Talalay et al., 1995). Oltipraz was reported to induce the transcription of CYP1A1 in rat tissues and in human colorectal cancer cell line Caco-2 cells, without physically binding the AhR (Le Ferrec et al., 2002). Chelating intracellular calcium by BAPTA-AM completely abolished the oltipraz-induced expression of CYP1A1, identifying calcium as a key regulator of CYP1A1 gene expression (Le Ferrec et al., 2002), however, no direct mechanism has been proposed.

On the other hand, in vitro studies have shown the AhR to be a substrate for the calcium-dependent protease calpain (Poland and Glover, 1988). Calpain, which is a family of cytosolic calcium-dependent cysteine proteases, is involved in regulating many cellular processes including proliferation, differentiation, cell motility and metastasis through regulation of signal transduction and cleavage of many target cellular regulatory proteins (Schoenwaelder et al., 1997; Potter et al., 1998; Carragher et al., 2002; Rios-Doria et al., 2004; Harwood et al., 2005). There are several calpain isoforms, however calpain I (μ -calpain), and calpain II (m-calpain) are ubiquitous isoforms, which requires either low or high calcium concentrations for activation, respectively. In this study a hypothesis was tested that activation by oltipraz of the AhR to induce CYP1A1 is mediated through the calcium-activated calpain.

2. Materials and methods

2.1. Materials

Calpain inhibitor III (MDL 28170) was purchased from Calbiochem (San Diego, CA). Tissue culture media and high-grade reagents were purchased from Sigma–Aldrich (St. Louis, MO). Dioxin (TCDD) was purchased through NCI Chemical Carcinogen Repository—Midwest Research Institute (Kansas City, MO). Epidermal growth factor, cholera toxin, fetal bovine serum, bovine pituitary extract, and Trizol reagent were purchased from Invitrogen (Carlsbad, CA). The random primers, Moloney murine leukemia virus (M-MLV) reverse transcriptase, RNasin, Taq polymerase, deoxyribonucleotide triphosphates (dNTPs), horseradish peroxidase (HRP)-conjugated goat anti-mouse immunoglobulin (IgG) and HRP-conjugated goat anti-rabbit IgG were purchased from Promega (Madison, WI). FITC-conjugate donkey anti-rabbit secondary antibody was purchased from Jackson Immunoresearch laboratories (West Grove, PA). The BCA Protein Quantification Kit was purchased from Pierce Chemicals (Rockford, IL). The calpain substrate *t*-butoxycarbonyl-Leu-Met-7-amino-4-chloromethylaminocoumarin (BOC-LM-CMAC) and Fluo-4-AM were purchased from Molecular Probes (Eugene, OR). Real time PCR kit was purchased from Bio-Rad (Hercules, CA). The rabbit polyclonal anti-AhR (BEAR 3 and BEAR 4) antibodies (Poland et al., 1990; Pollenz et al., 1994) were a kind gift from Dr. Christopher Bradfield, University of Wisconsin (Madison, WI). The Sager MT-2 metastatic cell line was derived from a patient with an infiltrating and intraductal carcinoma medium (Band et al., 1990), and was kindly provided by Dr. Vilma Band from Northwestern University (Chicago, IL). The mouse hepatoma cell line, Hepa-1c1c7 was provided by Dr. Lynn Allen-Hoffmann (University of Wisconsin Madison, WI).

2.2. Cell culture and treatments

The human breast cancer cell line MT-2 cells were cultured in DFCI media containing 1% FBS medium (Band et al., 1990), and the mouse hepatoma cell lines, Hepa-1c1c7 were grown in DMEM-F12 supplemented with 5% heat-inactivated FBS. For experiments, cells were seeded in six-well plates at a density of 5×10^5 and grown for 24 h. Cells were pre-incubated with calpain inhibitor MDL 28170 or dimethyl sulfoxide (DMSO) (0.1%) for 1 h and then simultaneously treated with either oltipraz (50 μ M) or TCDD (1 nM) for an extra 3 h. The vehicle used for MDL 28170, TCDD and oltipraz was DMSO, at 0.1% final concentration.

2.3. Immunocytochemical staining and fluorescence microscopy

Most of the experiments in this research were done on the MT-2 human breast cancer cell lines. However, due to the high levels of AhR associated with nuclear sites in the metastatic

MT-2 cells, the experiments investigating the ligand-induced AhR nuclear translocation were performed on Hepa-1c1c7, a murine hepatoma cell line, which has no constitutive nuclear AhR, and is well characterized for studying the AhR signaling. Hepa-1c1c7 cells were seeded at 10^5 on cover slips in six-well plates and allowed to grow for 24 h, then were pre-treated with calpain inhibitor MDL 28170 or DMSO (0.1%) for 1 h and then simultaneously treated with either oltipraz (50 μ M) or TCDD (1 nM) for an extra 1 h. Treatment media were removed and cells growing on cover slips were washed in cold PBS and then fixed by incubation in a (1/1) methanol/acetone solution at 4 °C for 30 min and subsequently air-dried and stored frozen at –20 °C air-tight, until immunostaining.

For immunostaining, cells grown on cover slips were first brought to room temperature, rinsed with TBST (10 mM Tris–HCl, 150 M NaCl, 0.05% Tween-20) and transferred to clean six-well plates. The cells on cover slips were incubated at room temperature for 1 h in 4% milk solution in TBST to block non-specific binding. The cover slips were then incubated at room temperature while rocking for 1 h in 1 μ g/ml anti-AhR polyclonal (BEAR-4) antibody in 2% milk solution in TBST. Cover slips were then washed three times (15 min each) with TBST. A 1:200 dilution of fluorescein isothiocyanate (FITC)-conjugated goat anti-rabbit antibodies in TBST containing 2% milk was added to the cover slips in reduced light. The cover slips were allowed to incubate with this secondary antibody at room temperature for 1 h. The cover slips were then washed extensively (3 \times for 15 min each in TBST; 3 \times for 10 min each in TBS). The cover slips were mounted on glass slides using mounting solution containing DABCO as a fluorescence anti-fading agent.

AhR immunostaining was scored at 200 \times magnification on the basis of the approximate number of cells with cytoplasmic or nuclear AhR staining relative to the total number of cells in the optical field. The percentages of cells with strong cytoplasmic or nuclear AhR staining were recorded in all optical fields and the mean percentage value was used to characterize the AhR subcellular localization as cytoplasmic or nuclear, respectively. Six consecutive microscope fields were analyzed for each slide. The percentages from different experiments were calculated and the mean of two independent experiments was plotted.

2.4. Preparation of total cell protein lysates and immunoblotting analysis

Following different treatments, cell monolayers growing in six-well plates were lysed in Trizol, which allowed for simultaneous isolation of RNA and protein as described previously (Eltom et al., 1999). The protein pellets were resuspended in 2% SDS and sonicated briefly to dissolve protein pellets and form lysates of total cellular extract. The protein concentration in cell extracts was determined using the BCA kit, per the manufacturer instructions (Pierce, Rockford, IL). Equivalent amounts of protein (10 μ g) were separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)

and transferred to polyvinylidene fluoride (PVDF) membranes (Eltom et al., 1999). The membranes were blocked at room temperature for 1 h in 4% non-fat milk in TBST with subsequent incubation with 1 μ g/ml anti-AhR (BEAR-3). After brief washing the blots were incubated with the corresponding HRP-coupled anti-rabbit (1:20,000) for 1 h followed by additional washing in TBST and TBS. Reactive protein bands were visualized using enhanced chemiluminescence reagents (Pierce Chemicals, Rockford, IL). Immunoreactive bands of AhR were quantified by AlphaMager 2000 Digital system using Alpha Image Acquisition Analysis Software (Alpha Innotech Corp, San Leonadro, CA). Subsequently, blots were probed with actin monoclonal antibody (1:4000) followed by anti-mouse secondary antibody (1:20,000) for normalization of protein loading. The levels of AhR protein were then divided by the corresponding levels of actin to generate normalized values for the concentration of AhR in each sample.

2.5. Reverse transcriptase polymerase chain reaction (RT-PCR)

Total RNA isolated from Trizol lysates was used to synthesize first strand cDNA using random hexamer primers and MMLV reverse transcriptase. To avoid genomic DNA contamination during PCR, all PCR primers were designed to overlap more than two exons. Human CYP1A1 PCR amplification was done using forward primer sequence 5'-CTA TGA CCA CAA CCA CCA AGA ACT G-3' and the reverse primer sequence 5'-AGG TAG CGA AGA ATA GGG ATG AAC TC-3', which yield a product of 111 bp between exon 5 and 6. The mouse CYP1A1 was amplified using primers (forward primer, 5'-GCC TTC ATT CTG GAG ACC TTC C-3'; reverse primer, 5'-CAA TGG TCT CTC CGA TGC-3'), giving a product of 280 bp between exon 5 and 7 of the mouse *Cyp1a1* gene (Wei et al., 2004). House keeping gene glyceraldehyde 3-phosphate dehydrogenase (GAPDH) was amplified as an internal control using forward primer 5'-ACC ACA GTC CAT GCC ATC AC-3' and reverse primer 5'-TCC ACC ACC CTG TTG CTG TA-3' while the housekeeping gene 18S was amplified using 5'-CGG ACA GGA TTG ACA GAT TGA TAG C-3' forward primer and reverse primer 5'-TGC CAG AGT CTC GTT CGT TAT CG-3'. CYP1A1 was amplified for 30 cycles, and GAPDH and 18S for 20 cycles, each cycle with the following segments: 1 min at 95 °C, 1 min 30 s at 60 °C, and 2 min at 72 °C. PCR products were separated on agarose gels and visualized with ethidium bromide. The bands were quantified using the NIH ImageJ software (Version 1.36) for image analysis.

2.6. Intracellular calcium measurements

MT-2 cells cultured in 24-well plates (2×10^5) in DFCI media were loaded with 5 μ M Ca^{2+} -sensitive dye Fluo-4-AM (Molecular Probes, Eugene, Oregon) for 45 min at 37 °C. Following the pre-incubation, the cells were rinsed three times with DFCI media to remove any free dye and then incubated for a further 30 min period in media alone to allow complete

de-esterification of AM esters. Fluo-4-loaded cells were then stimulated with 10 nM TCDD, 50 μ M oltipraz, or their vehicle DMSO. Changes in intracellular calcium were measured as captured fluorescence images of cells at 25 min, using the IX50 Olympus Fluorescence microscope (excitation at 385 nm, emission at 512 nm). Relative fluorescence values were quantified using the NIH ImageJ software for image analysis (Version 1.36) and translated into calcium units.

2.7. Calpain activity assay

Calpain activity in intact MT-2 cells was determined by measuring the hydrolysis of the calpain specific peptide substrate BOC-LM-CMAC, which was assessed by fluorescence microscopy as described previously (Glading et al., 2001) with the excitation and emission wavelengths 350 and 430 nm, respectively. The non-fluorescent cell-permeable substrate is conjugated by intracellular thiols into a membrane impermeable form allowing substrate accumulation within the cell (Carragher et al., 2004; Rosser et al., 1993), and proteolytic cleavage of this peptide by calpain produces chloromethylaminocoumarin (CMAC) which possesses blue fluorescence. MT-2 cells were treated with either 50 μ M or 100 μ M oltipraz for 1 h. Cells were then incubated at 37 °C for 20 min in the presence of 50 μ M BOC-LM-CMAC. The cells were observed for CMAC fluorescence corresponding to calpain activity with an Olympus IX50 fluorescence microscope. The image exposure settings were identical within each experiment. Fluorescence of the images was quantified by using the NIH ImageJ software (Version 1.36), a Java image-processing program, which analyzes the pixel value of the fluorescent images.

2.8. Statistical analysis

The data generated from different experiments were analyzed using GraphPad Prism Software (San Diego, CA) by one-way analysis of variance ANOVA and Tukey-Kramer multiple comparison tests of control values with treated. Changes were deemed significant if $p \leq 0.05$.

3. Results

3.1. Oltipraz-induced calcium mobilization

Previous reports have demonstrated the ability of oltipraz to increase intracellular calcium in human colorectal carcinoma cells (Le Ferrec et al., 2002) in a concentration dependent manner. Therefore, it was important to first determine if oltipraz would affect the intracellular calcium in our study cell system, the metastatic MT-2 human breast cancer cell line. The data presented in Fig. 1. A illustrate the ability of oltipraz to mobilize calcium in a concentration-dependent fashion. The increase in calcium occurs instantaneously after the addition of the drug. Thus, oltipraz rapidly increases intra-

cellular calcium in MT-2 cells to a comparable extent to the effect of Ionomycin, the calcium ionophore.

3.2. Calpain activity analysis following increases in $[Ca^{2+}]_i$

To further assess the oltipraz-induced change in intracellular calcium on calpain activation a cell-permeable highly specific calpain substrate, BOC-LM-CMAC was utilized. The blue fluorescence of the calpain-cleaved product detected with the Olympus IX50 wide field fluorescence microscope is indicative of calpain activation. Oltipraz exposure for 1 h resulted in a significant increase in calpain activity indicated by the intense blue fluorescence (Fig. 1B) when compared to the DMSO control group, suggesting that oltipraz has the capacity to activate calpain. More importantly, calpain activation seen with oltipraz is concentration dependent. These results suggest that oltipraz is responsible for the activation of calpain through its ability to increase intracellular calcium concentrations.

3.3. Ligand-independent activation of the AhR by oltipraz

3.3.1. Nuclear translocation

Since it was previously shown that oltipraz could activate AhR to induce CYP1A1 expression without binding the AhR, we set to investigate the effect of oltipraz on the signaling pathway of the AhR activation. Following binding of ligand (such as TCDD) to AhR, the receptor is activated and it acquires the ability to translocate from the cytoplasm into nuclear sites where it functions as a transcriptional enhancer for many genes including CYP1A1. Therefore, the ability of oltipraz to facilitate the nuclear translocation was investigated here in comparison to TCDD, the most potent agonist for AhR. The data in Fig. 2 remarkably have shown that oltipraz was capable of evoking nuclear translocation of AhR within 1 h to almost the same extent as TCDD, resulting in nuclear translocation of AhR in approximately 70% of Hepa-1c1c7 cells, compared to 75% in TCDD-treated cells.

To investigate the role of oltipraz-induced calpain activation in this process, the potent calpain-specific inhibitor, MDL 28170 was used to block calpain and the effect of oltipraz was further examined. Pre- and co-treatment of Hepa-1c1c7 cells with MDL 28170 has resulted in a complete inhibition of oltipraz-induced nuclear translocation of AhR (Fig. 2). Similarly, MDL 28170 was capable of blocking TCDD-induced nuclear translocation of AhR, indicating that calpain is probably

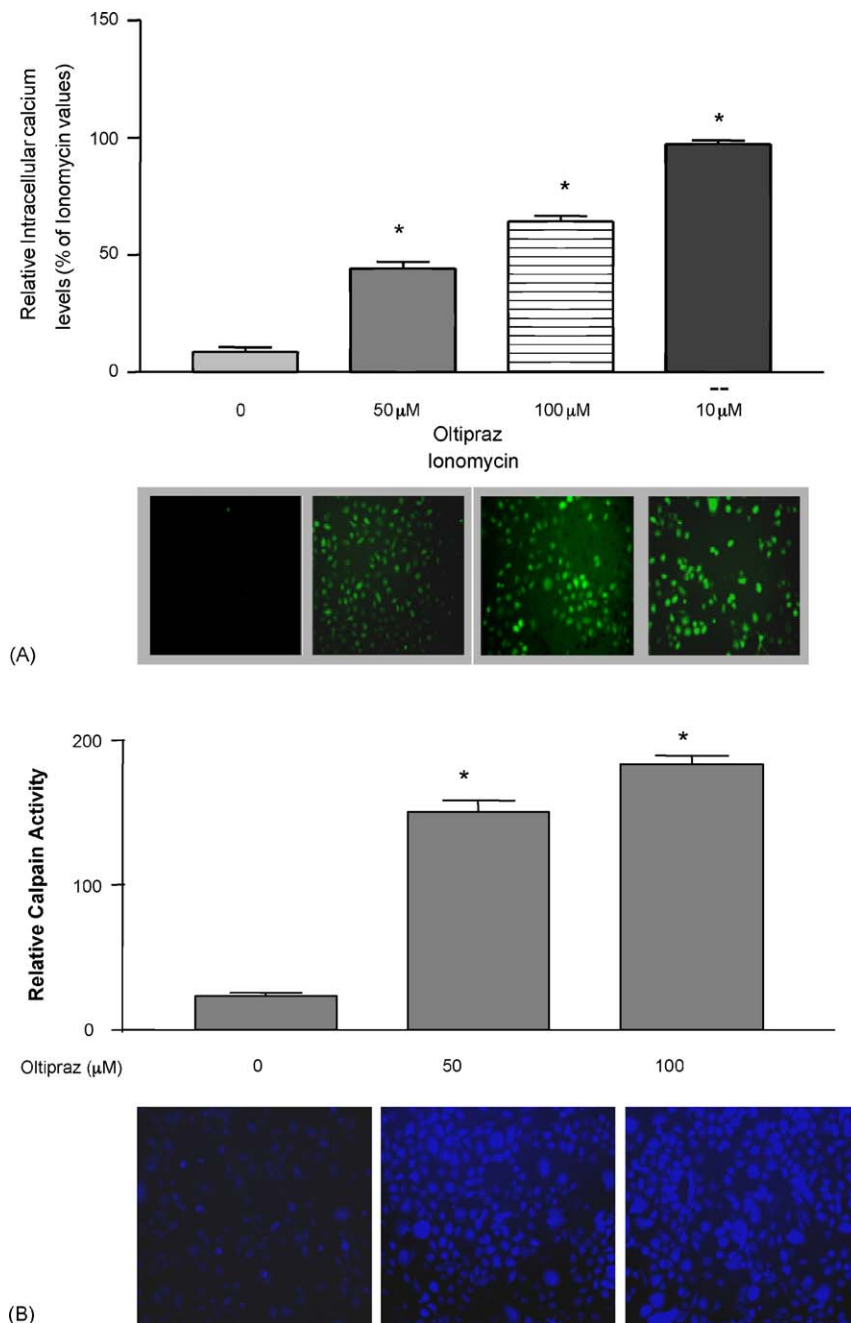


Fig. 1. (A) The effect of oltipraz on intracellular free calcium concentration in MT-2 cells. MT-2 cells were pre-loaded with 5 μ M Fluo-4-AM for 45 min at 37 °C (as described in Section 2). The Fluo-4 loaded cells were then stimulated with 50 μ M or 100 μ M oltipraz, 10 μ M Ionomycin (positive control), or their vehicle DMSO. Changes in intracellular calcium were measured as captured fluorescence images of cells over a period of 40 min (every 5 min), using the IX50 Olympus Fluorescence microscope (excitation at 385 nm, emission at 512 nm). Relative fluorescence values for the peak calcium concentration at 25 min were quantified from several fields using the ImageJ software, and graphed values are means and standard deviations of three independent experiments. The lower panel is a representative of the images quantified. * $p < 0.05$, comparing drug treatments to vehicle control. (B) Activation of calpain in MT-2 cells following exposure to different concentrations of oltipraz. Calpain activity was analyzed in MT-2 cells exposed for 1 h to 50 and 100 mM oltipraz or its vehicle DMSO using peptide substrate BOC-LM-CMAC. Blue fluorescence of the calpain-cleaved substrate, corresponding to calpain activity was captured over time (20 min) by fluorescence microscopy (100 \times magnification). The fluorescence intensity of the images were quantified using the ImageJ software from several fields, and plotted values are the mean and S.D. of $n = 3$ independent experiments. * $p < 0.05$, comparing oltipraz treatments to vehicle control.

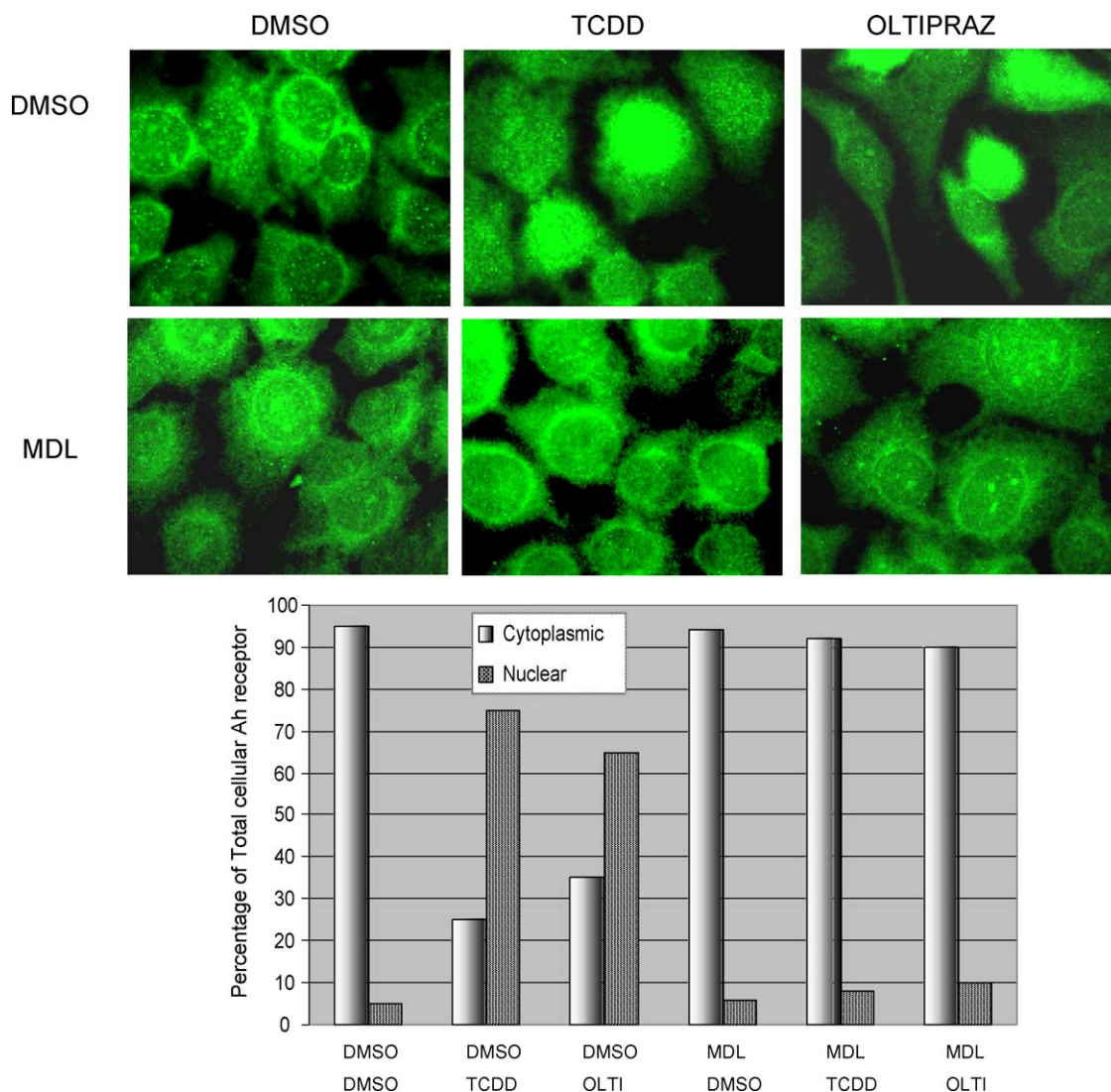


Fig. 2. The effect of oltipraz on the subcellular localization of AhR in Hepa-1 cells. Murine Hepa-1c1c7 cells grown on cover slips were pre-treated with calpain inhibitor, MDL 28170 (30 μ M) or its vehicle DMSO for 1 h, then exposed for 1 h to 50 μ M oltipraz, 1 nM TCDD (as a positive control) or their vehicle DMSO. Cells were fixed and immuno-stained for AhR followed by FITC-conjugated secondary antibodies as described in Section 2. Cells were viewed using the IX50 Olympus Fluorescence microscope and scored for cytoplasmic and nuclear staining from multiple fields, as described in Section 2. Average numbers from different experiments were normalized to a percentage, and the average of two independent experiments was graphed. A representative of the cellular staining for AhR is presented in the upper panel.

mediating this step for both chemicals, in spite of the difference in their mode of action on the AhR activation.

3.3.2. Enhanced transcription of CYP1A1

To assess the ability of oltipraz to increase the transcriptional activity of AhR, the expression of CYP1A1 mRNA as an endpoint was analyzed by RT-PCR. Data in Fig. 3 demonstrate that treatment of MT-2 cells with oltipraz for 6 h has resulted in a concentration dependent induction of CYP1A1 mRNA, in agreement with the previous reports (Le Ferrec et al., 2002).

3.4. Inhibition of oltipraz-induced CYP1A1 expression by the calpain inhibitor, MDL 28170

3.4.1. In the metastatic MT-2 human breast carcinoma cell line

To investigate whether calpain is involved in the oltipraz-induced expression of CYP1A1 in MT-2 cells, they were pre- and co-treated with the calpain potent inhibitor, MDL 28170 then challenged with oltipraz for 3 h. The data collected from multiple experiments on this cell line have clearly established that although

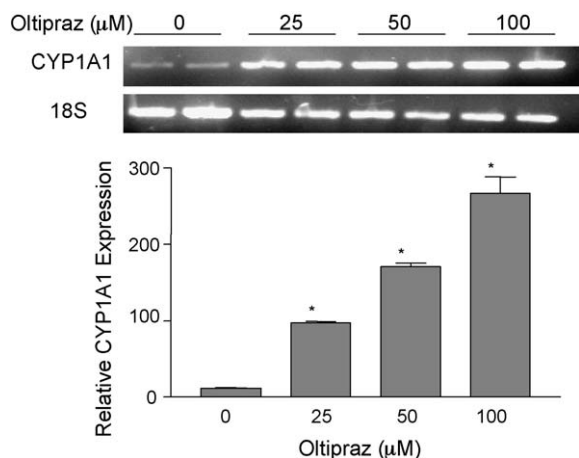


Fig. 3. RT-PCR analysis of the CYP1A1 expression following treatment of MT-2 cells with increasing doses of oltipraz. MT-2 cells were treated with 25, 50 and 100 μ M oltipraz for 6 h. RNA was isolated from the treated cells, cDNA was prepared by reverse transcriptase reaction (RT) and CYP1A1 mRNA expression was measured using conventional PCR. Ribosomal 18S was amplified as an internal control and their values were used to normalize CYP1A1 values. The bars represent the average \pm S.D. for three independent experiments assayed in duplicates. A * p < 0.05, relative to DMSO control group. A representative of a gel of one PCR analysis is presented as an illustration in the top panel.

oltipraz alone has induced CYP1A1 substantially over the vehicle-treated control, the co-treatment with the calpain inhibitor completely blocked this induction and brought the CYP1A1 to the DMSO-treated control levels (Fig. 4).

3.4.2. In Hepa-1c1c7 murine hepatoma cell line

To eliminate the possibility that this phenomenon is cell-specific, the same experiment was repeated using the mouse hepatoma cell line Hepa-1c1c7. Similarly, oltipraz alone has induced CYP1A1 substantially over the DMSO-treated control to a similar extent as TCDD, the positive control, and co-treatment with the calpain inhibitor MDL 28170 completely blocked this induction (Fig. 5).

3.5. Down-regulation of the AhR by oltipraz

In the well-established AhR signaling cascade, binding of a ligand to AhR will activate it to translocate to the nucleus, where it dimerizes with its partner ARNT to bind XRE of the enhancer region of AhR-responsive genes, such as CYP1A1 gene and enhances their transcription. Following the transcriptional activation, the AhR undergoes a massive depletion (Prokipcak and

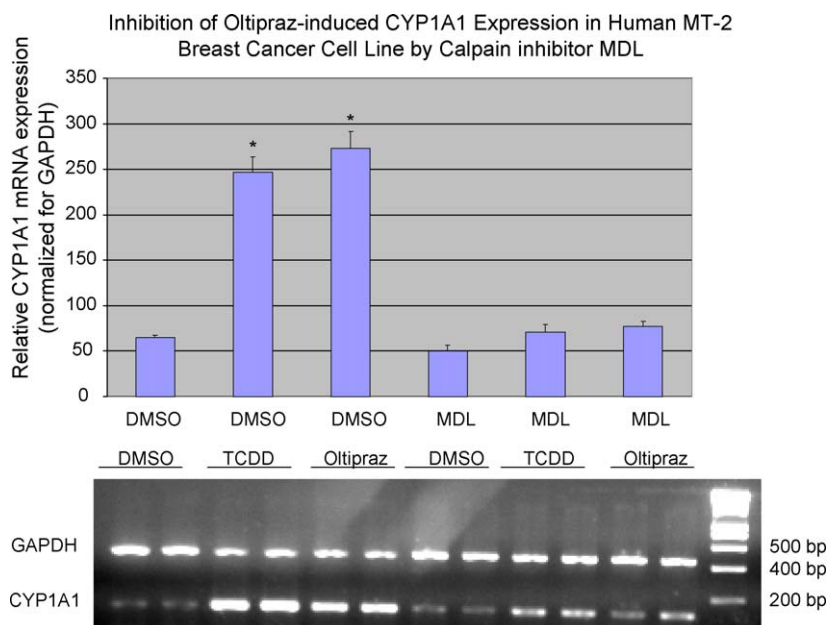


Fig. 4. Inhibition of oltipraz-induced CYP1A1 expression by MDL 28170, Calpain inhibitor in MT-2, human breast cancer cell line. MT-2 cells were pre-treated with calpain inhibitor, MDL 28170 (30 μ M) or its vehicle DMSO for 1 h, then exposed for 3 h to 50 μ M oltipraz, 1 nM TCDD (a positive control) or their vehicle DMSO. RNA was isolated from the treated cells and analyzed by RT-PCR as described in Section 2. GAPDH was amplified as an internal control and its value was used to normalize CYP1A1 values. The bars represent the average \pm S.D. for three independent experiments of duplicate cultures, which were PCR-assayed in duplicates. A * p < 0.05, relative to DMSO control group. A representative gel image of one PCR analysis is presented in the lower for illustration.

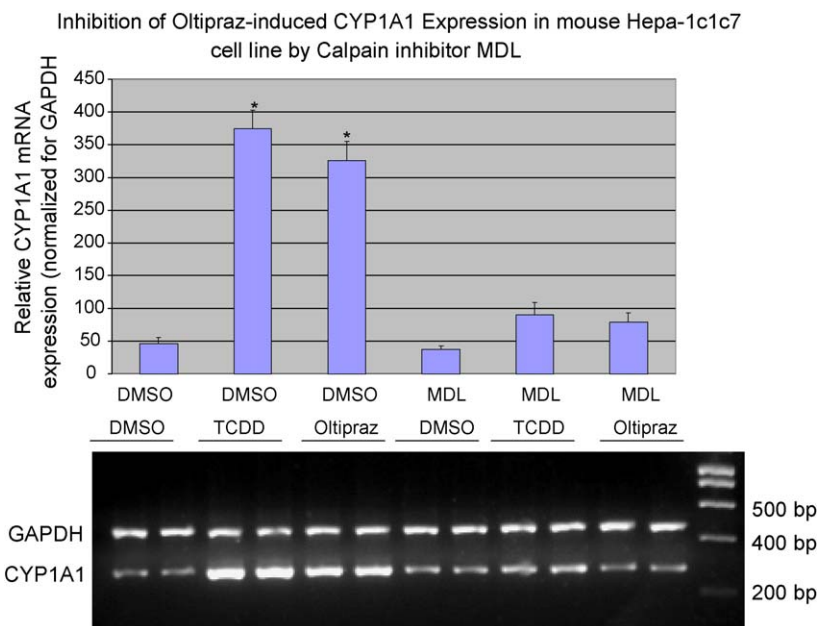


Fig. 5. Inhibition of oltipraz-induced CYP1A1 expression by MDL 28170 Calpain inhibitor in Hepa-1, murine hepatoma cell line. Hepa-1 cells were pre-treated with calpain inhibitor, MDL 28170 (30 μ M) or its vehicle DMSO for 1 h, then exposed for 3 h to 50 μ M oltipraz, 1 nM TCDD (a positive control) or their vehicle DMSO. RNA was isolated from the treated cells and analyzed by RT-PCR as described in Section 2. GAPDH was amplified as an internal control and its value was used to normalize CYP1A1 values. The bars represent the average \pm S.D. for three independent experiments of duplicate cultures, which were PCR assayed in duplicates. A * p < 0.05, relative to DMSO control group. A representative gel image of one PCR analysis is presented in the lower panel for illustration.

Okey, 1991; Roberts and Whitelaw, 1999). It was of interest to investigate whether oltipraz would induce this down-regulation of AhR, even though it is not a ligand for the receptor. Data in Fig. 6 illustrate that, indeed, exposure to oltipraz for 6 h results in a substantial reduction in AhR protein, while the levels of actin, the house-keeping protein were not affected by the treatments. The oltipraz-induced depletion of AhR was a concentration dependent, where a 25 μ M of oltipraz has resulted in 50% reduction of the receptor in comparison to the DMSO-treated control cells. In addition, treatment with 50 μ M oltipraz has caused a 75% reduction in the AhR while 100 μ M oltipraz resulted in >90% reduction in the receptor level.

Clearly, these data suggests that oltipraz down-regulates the AhR in a concentration dependent manner, which may be attributed to its effect in elevating intracellular calcium and subsequent activation of calpain enzymatic activity, which were established earlier in this study (Fig. 1).

4. Discussion

Oltipraz has been developed as a chemopreventive agent for many malignancies, including liver and colorectal cancers, on the basis of its *in vivo* protective activ-

ity against chemically induced tumors, in a variety of animal models. This protection has been associated with an enhanced capacity to detoxify reactive carcinogens and, more recently, with increased DNA repair (Kensler et al., 1987; Talalay et al., 1995; O'Dwyer et al., 1997). The ability of oltipraz to induce both phase I and phase II drug metabolizing enzymes has been reported, however CYP1A1 seems to be among the most sensitive of all these enzymes. While most enzymes in Phase II group are detoxifying enzymes, which underlies the protective effect of oltipraz, CYP1A1 is involved in bioactivation of a number of carcinogens, including PAH and endogenous hormones such as estrogen.

Previous reports and our present study have established that oltipraz induces CYP1A1 transcription in an AhR- and calcium-dependent fashion (Le Ferrec et al., 2002). In this report we present evidence that calcium-dependent calpain is involved in mediating this induction by coupling the oltipraz-induced elevation of intracellular calcium and the activation of AhR. Although the increase in the intracellular calcium by oltipraz is the trigger that was identified previously to cause the activation of AhR to induce CYP1A1, the steps leading to the activation were not identified. It was proposed that $[Ca^{2+}]_i$ could mediate such a response by activating protein kinase C or other kinases to activate the AhR,

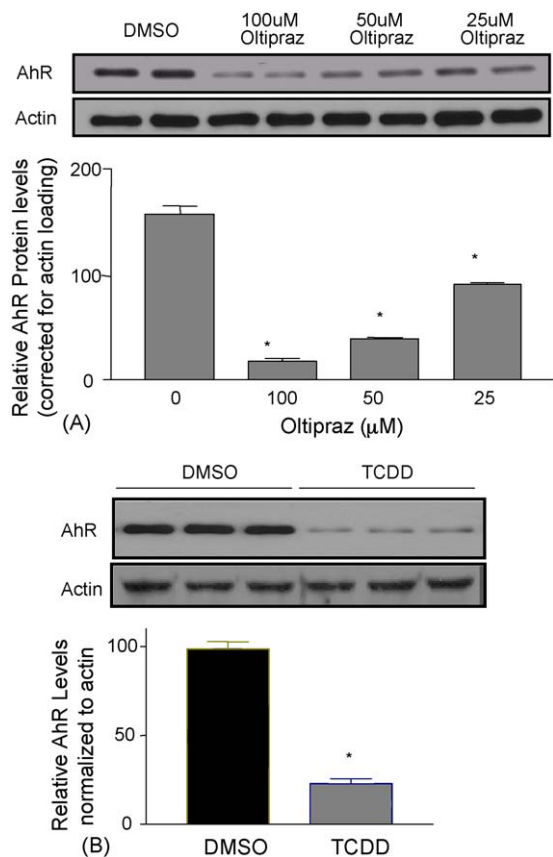


Fig. 6. Stimulation of down-regulation of the AhR protein by treatment with increasing doses of oltipraz. (A) MT-2 cells were exposed to varying concentrations of oltipraz for 6 h and total cellular proteins were analyzed for AhR protein levels. The relative expression of AhR was quantified by densitometric quantitation of AhR band and normalized to the level of actin. The bars represent the average \pm S.D. for three independent experiments. (B) Western blot analysis of AhR protein levels in MT-2 cells exposed to TCDD. Triplicate cultures of MT-2 cells were exposed to either TCDD (1 nM) or its vehicle (DMSO) for 3 h. The relative expression of AhR was quantified by densitometric quantitation of AhR band and normalized to the level of actin. The bars represent the averages for two independent experiments. A * $p < 0.05$, comparing treatment groups to DMSO control group.

however, previous studies have demonstrated that AhR is constitutively phosphorylated and no additional phosphorylation was observed upon its activation (Berghard et al., 1990; Pongratz et al., 1992).

The present study provides evidence that activation of calpain by oltipraz contribute to each of the sequential steps of the AhR signaling pathway leading to its transcriptional activation of CYP1A1. Previous studies have already established that oltipraz does not bind to the AhR, however, the next step following the ligand binding is the receptor transformation, which is the acquisition by the receptor of the ability to translocate from the cyto-

plasm to the nucleus and bind DNA and enhance transcription. Data presented here, clearly demonstrate that oltipraz is capable of inducing AhR nuclear translocation, through activation of calpain by means of increasing the intracellular calcium. It is given that the accumulation of AhR in the nucleus requires the tight binding of AhR (and its partner ARNT) to the XRE of the responsive genes.

Subsequently, oltipraz treatment has induced the expression of CYP1A1 within 3 h, and in a concentration-dependent manner, with concentrations ranging from 25 to 100 μ M. Remarkably, blocking of calpain by MDL 28170 has completely abolished this induction in both the human breast cancer cell line and the murine hepatoma cell line, indicating that this phenomenon is not cell type- or species-specific.

In the final step in the AhR signaling pathway, following the transcriptional activation, the AhR exits the nucleus and undergoes a massive depletion within hours of ligand binding (Giannone et al., 1998; Harper et al., 1994; Prokipcak and Okey, 1991; Pollenz, 1996; Roberts and Whitelaw, 1999). The data presented in this report indicate that oltipraz through activation of calpain does indeed down-regulate AhR in a concentration-dependent fashion, and in a comparable magnitude to the most potent AhR agonist, TCDD.

Collectively, the data presented in this report provide evidence for the first time for involvement of calpain in mediating the oltipraz-induced expression of CYP1A1 and in activating AhR signaling pathways.

Acknowledgements

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Overexpression of the Aryl Hydrocarbon Receptor Induces Malignant Transformation in Mammary Epithelial Cells

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Abstract

Introduction

The aryl hydrocarbon receptor (AhR), which mediates toxic and carcinogenic responses to environmental polycyclic aromatic hydrocarbons (PAH), is a ligand activated basic helix-loop-helix transcription factor. The AhR has been shown to interact with a number of proteins known to regulate the cell cycle, which provides further implications for its role in cancer. There is ample documentation of the role of AhR in PAH-induced carcinogenicity. However, in this report we addressed whether overexpression of AhR alone is sufficient to induce carcinogenic transformation in human mammary epithelial cells (HMEC).

Methods

Retroviral expression vectors were used to develop a series of stable cell lines expressing varying levels of AhR protein in an immortalized normal HMEC with relatively low endogenous AhR expression. Each cell line was characterized for AhR expression and transcriptional activity as well as phenotypic changes associated with malignancy. The increase in AhR activity and expression was correlated with the development of malignant phenotypes.

Results

Clones overexpressing AhR by 3-fold manifested a 50% decrease in population doubling time compared to vector-control cells. Cell cycle analysis revealed that this enhancement in proliferation was mainly due to an increase in the percentage of cells transiting from G0/G1 to S- and G2/M phases. Overexpression of AhR enhanced the motility of HMEC and increased their migration by ~60% compared to their vector-expressing clones. More importantly, these cells acquired the ability to invade matrigel matrix, where more than 80% of plated cells invaded the matrix and crossed the membranes within 24 h, whereas none of parental or the vector control HMEC was able to invade

Appendix 9

matrigel. These malignant phenotypes were also coupled with the ability of the clones to form colonies in soft agar.

Conclusion

Collectively, these data provide the first evidence for a direct role of AhR in the progression of breast carcinoma. The results suggest a novel therapeutic target that should be considered for treatment and prevention of progression of this disease.

Introduction

The aryl hydrocarbon receptor (AhR) is a basic helix-loop-helix (bHLH) transcription factor [1] that is well characterized for mediating the carcinogenic responses to environmental polycyclic aromatic hydrocarbons (PAH), such as 2,3,7,8-tetrachloro-dibenzo-*p*-dioxin (TCDD) [2, 3]. Binding of PAH to AhR in the cytoplasm leads to its activation and subsequent translocation into the nucleus, where it dimerizes with another bHLH protein, the AhR nuclear translocation protein (ARNT). This heterodimer binds to xenobiotic responsive elements (XRE) in the enhancer region of PAH-responsive genes such as cytochrome P450 1A1, *CYP1A1*, and enhances their transcription [4-6]. No physiological function has been established for any of the identified endogenous ligands of AhR [7, 8]. However constitutive activation of AhR via disturbing cellular adhesion to extracellular matrix [9], increasing intracellular calcium [10] or disturbing cytoskeleton [11] has suggested that pathophysiologically-activated pathways are operating to regulate the receptor.

Exposure to TCDD in animals induces teratogenesis, immuno-suppression, reproductive defects and tumor promotion in an AhR-dependent manner [12-16]. TCDD-dependent activation of AhR has also been linked to enhanced-terminal differentiation in keratinocytes and adipocyte [17, 18]. Moreover, AhR null mice generated by two independent laboratories exhibit a spectrum of hepatic and immune system defects [19, 20] and are resistant to benzo[a]pyrene-induced carcinogenicity [21], providing evidence to link AhR to normal development and tissue homeostasis.

In cultured cells activation of AhR by TCDD inhibits cell cycle progression arresting cells at the G1/S checkpoint through induction of cyclin-dependent kinase inhibitor p27^{kip1} [22]. This effect on cell cycle progression relies on a direct protein-protein interaction between AhR and retinoblastoma (Rb) through two LXCXE domains on the AhR [23]. This association with Rb was shown to require

AhR activation and nuclear translocation [24]. Interestingly, the AhR in the absence of a ligand was shown to influence the cell cycle progression, cell shape and differentiation [25, 26].

A series of previous findings prompted the present studies. First, TCDD acting through AhR has been shown to exert a strong anti-mitogenic effect in estrogen-responsive tissues and to exhibit a broad spectrum of anti-estrogenic activities in human breast carcinoma cell lines [27-29]. Second, the AhR null mouse exhibits impaired development of mammary gland ductal branching [30], suggesting a role for AhR in regulating proliferative stages required for mammary gland development. Our own data have demonstrated that the expression of the AhR is elevated in direct proportion to the tumor progression in both human breast carcinoma cell lines and breast tumors [31]. This study was undertaken to investigate whether induced overexpression of AhR could be both necessary and sufficient for development of transformed phenotypes in human breast epithelial cells.

Material and Methods

Cells and culture conditions

The H16N2 immortalized human mammary epithelial cell line and the metastatic MT2 breast cancer cell line were kindly provided by Dr. Vilma Band (Northwestern University, Chicago, IL). MT2 cells, H16N2 cells and the subsequently generated clones were grown in DFCI-1 media as described [32] and were maintained in culture at 37°C and 5% CO₂.

Recombinant retroviral expression vector and virus production

The human AhR cDNA was provided by Dr. Chris Bradfield (McArdle Laboratory for Cancer Research, Madison, WI). Bgl II (5') and Cla I (3') restriction sites were added to the full length AhR by PCR to generate a fragment with compatible cloning sites for ligation into the pLNCX2 retroviral vector (Retro-X-System from BD Biosciences), under control of the human cytomegalovirus early promoter (pCMV). This vector also contains a neomycin resistance gene under the viral LTR

Appendix 9

promoter to allow for selection in mammalian cells. The sequences of retroviral vectors containing the human AhR cDNA (ret-AhR) or the corresponding empty vector control (EV), were confirmed by DNA sequencing at the Vanderbilt-Ingram Cancer Center Molecular Biology Core Facility (Nashville, TN). The two vectors were transfected independently into the Phoenix packaging cell line by calcium phosphate method to produce infectious viral particles, following the manufacturer's instructions. Equal amounts of the pBMN-I-GFP retro vector DNA were co-transfected with each vector to provide a visible screenable marker to assess the transfection efficiency. The titer of the viral stock was assayed using mouse embryo fibroblasts (MEF) generated in this laboratory from AhR-null mice.

Development of stable cell lines

H16N2 cells were plated at 2×10^6 per 6-cm plate and allowed to incubate overnight. Viral supernatants were mixed with culture media and added to the H16N2 cells in the presence of polybrene (4 μ g/ml) with gentle and thorough mixing. Cells were incubated at 37°C for 12-18 hours, viral medium was then removed and fresh medium was added to cells for an extra 24-48h, when the fluorescence of GFP was observed under fluorescence microscope.

Selection, cloning and expansion of clones:

H16N2 stable transfectants harboring the retro-AhR or EV control vector were isolated by G418 antibiotic selection. The optimal antibiotic concentration was determined as 800 μ g G418/ml of medium and was added to the cells for one week, with fresh medium and antibiotic replenished every two days. Surviving cells were expanded and cloned by limited dilution. Briefly, cells were plated at 100 cells per 150mm plate surface. The position of individual attached cells was pinpointed on the under side of the culture dish using a marker. The cells were allowed to grow and expand for one week. Once the individual cells divided to form small colonies, sterile cloning discs pre-soaked in

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trypsin-EDTA were placed on each isolated colony. Cells from each disc were placed in an individual well of a 24-well plate and allowed to reach confluence. Each clone was then expanded and characterized for AhR protein expression by Western immunoblotting. Five clones, with varying AhR expression, and a clone of EV-expressing cell lines were selected for subsequent characterization.

Western Immunoblotting

Total proteins were isolated from Trizol (Invitrogen, Carlsbad, CA) lysates of cells per manufacturer's instructions and protein concentration was determined using BCA protein assay (Pierce, Rockford, IL). Proteins were separated on 7.5% SDS-PAGE and transferred to PVDF membranes. Membranes were first stained with Ponceau S (Sigma Chemicals, St Louis MO) to visualize protein bands to ensure equal protein transfer. Membranes were blocked with 4% milk in Tris-buffered saline containing 0.05% Tween 20 (TBST) for 1 hour. Membranes were then incubated with affinity-purified rabbit anti-AhR polyclonal antibody (BEAR-3) from Dr. Chris Bradfield (McArdle Laboratory for Cancer Research, Madison, WI) in 2% milk in TBST (1 µg/ml) for 1 hour. Membranes were rinsed 3x in TBST and followed by incubation for 1 hour in 1:20,000 dilution of horseradish peroxidase-conjugated anti-rabbit IgG in 2% milk solution in TBST (Promega, Madison, WI). Immunoreactive proteins were visualized using chemiluminescence reagents (Pierce Chemicals, Rockford, IL). To determine the relative expression of AhR protein among samples, band density was quantified by AlphaImager 2000 Digital system using Alpha Image acquisition analysis software (Alpha Innotech Corp, San Leonardo, CA). Subsequently, blots were re-probed with Actin monoclonal antibodies (1:4000) to normalize for protein loading.

Reverse Transcriptase-Polymerase Chain Reaction (RT-PCR)

Following cell lysis with Trizol, total RNA was isolated according to manufacturer's protocol. The cDNA was prepared from 2 µg of RNA using random hexamer primers and Moloney murine leukemia virus reverse

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transcriptase. CYP1A1 PCR amplification was done using forward primer sequence 5'TAG ACA CTG ATC TGG CTG CAG3' and the reverse primer sequence 5'GGG AAG GCT CCA TCA GCA TC3'. Glyceraldehyde 3-phosphate dehydrogenase, amplified using forward primer 5'ACC ACA GTC CAT GCC ATC AC3' and reverse primer 5'TCC ACC ACC CTG TTG CTG TA3', was used as an internal control.

Immunocytochemical staining and fluorescence microscopy

Cells growing on glass coverslips in 6-well plates were washed in cold PBS and fixed by incubation in a 1:1 methanol: acetone solution at 4°C for 30 minutes and then air dried. Fixed cells on coverslips were used for either staining immediately or stored airtight at -20°C until staining.

For immuno-staining, cells were rinsed and hydrated with TBST and transferred to a clean 6-well plate. The cells were incubated at room temperature for 1 hour in 4% milk solution in TBST to block nonspecific binding, followed by incubation at room temperature for 1 hour with affinity-purified rabbit anti-AhR polyclonal antibody (BEAR-4) in 2% milk solution in TBST (1 µg/ml) while rocking. Cells were then washed three times (15 min each) with TBST. Cells were incubated with a 1:200 dilution of fluorescein isothiocyanate (FITC)-conjugated anti-rabbit antibodies (Jackson ImmunoResearch laboratories, West Grove, PA) in 2% milk at room temperature for 1 hour. The cells were then washed extensively (4x for 15 min each in TBST, 3x for 10 min each in TBS, 2x for 10 min each in ddH₂O) and mounted on glass slides using PBS-glycerol supplemented with anti-fading agent (DABCO).

Cell proliferation studies

Proliferative capacity of the clones was determined using the FluoReporter Blue Fluorometric dsDNA Quantitation kit from Molecular Probes (Eugene, OR). This method measures cellular proliferation based on quantitation of cellular DNA using the blue-fluorescent Hoechst 33258 nucleic acid stain, with all manipulations carried out in 96-well plates. Serial dilutions of cells in 100ul

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culture media were plated in microplate wells, ranging from 1000 to 100,000 cells per well. The plates were allowed to incubate at 37° C for 3, 12, 24, 48, and 72 hours at which times the medium was removed and the plates were placed at -80°C. The plates were allowed to thaw and 100ul of distilled water was added to each well and the plate was incubated at 37°C for 1 hour. The plate was then placed at -80°C until frozen and then thawed to room temperature. A 100ul aliquot of aqueous Hoechst 33258 was added to each well. Fluorescence of Hoechst 33258 dye was measured on a Cytofluor using excitation and emission filters 360nm and 460nm, respectively.

Cell cycle analysis

Cells were trypsinized and single cell suspensions were fixed in cold 70% ethanol. Fixed cells were stored at -20°C until staining. Cells were harvested by centrifugation at 700 rpm for 5 minutes and resuspended in PBS. The cells were checked microscopically to ensure no clumps persisted. If clumps were observed, cells were passed 3-5 times through a 25-gauge syringe needle. RNase in PBS (0.1mg/ml) and propidium iodide (40 µg/ml) was added to the suspension. The cells were incubated at 37°C for 30 minutes. The fluorescent cells were then analyzed in a FACS Caliber BenchTop Analyzer (Becton-Dickson). The percentage of cell cycle distribution was determined using ModFit analysis software.

Invasion and migration studies

The invasive potential of the generated clones was measured by using a fluorescence-based tumor cell invasion assay (FluoroBlok invasion assay kits, BD Biosciences, Franklin Lakes, NJ). The assay has coupled a multi-well insert device containing a micro-porous membrane with a BD Matrigel coating process. The micro-porous membrane allows separation of fluorescence readings of the top and bottom compartment of the chamber. The BD Matrigel coat functions as a barrier to the passage of non-invasive cells analogous to the *in vivo* extracellular basement membrane.

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Cell suspensions were prepared by trypsinizing cell monolayers and resuspending the cells in serum-free medium at 5×10^4 cells/ml. Medium (750ul) containing 5% fetal calf serum was added to the bottom of each well as a chemo-attractant. A 500ul aliquot of the cell suspension (2.5×10^4 cells) was added to the top chamber. The cells were incubated at 37°C for 24 hours. Following incubation, the medium from the top chamber was carefully removed by aspiration and the insert was transferred to a second plate containing 0.5ml/well of 4µg/ml Calcein AM (Molecular Probes, Eugene, OR). The plates were allowed to incubate for 1 hour at 37°C. Calcein fluorescence of the invaded cells was read from the bottom at excitation and emission wavelength of 485 and 530 nm, respectively. The migration measurements were performed similar to the invasion assay procedure, with the exception that inserts *without* a matrigel coating were used, and migration was measured at three different cell densities.

Cloning in soft agar

A 0.6% agar underlay was prepared by combining an equal volume of 2X DFCI medium and 1.2% agar. The 0.6% agar was added to the bottom of 6-well culture plates and allowed to gel at room temperature. Cell suspensions of 1×10^4 cells/ml and 3.5×10^3 cells/ml were prepared and 20ul of each dilution were added to 2ml of 0.3% agar medium. The agar and cell suspensions were mixed and 1ml of each mixture was added to the respective wells. The solution was allowed to gel at room temperature. The culture plates were then stored in a 37°C incubator for 2 weeks and were fed every three days. Cells were plated in triplicate at each cell density.

Statistical analysis:

A two-tailed Student's t-test was used to compare the mean values of cell doubling times, migration, invasion or soft agar colonization between empty vector (EV)-carrying control cells and different clones overexpressing the AhR. A *p*-value of 0.05 or less was deemed significant.

Results

Overexpression of AhR is paralleled by transformation to a fibroblastic morphology

We developed five independent clonal cell lines over-expressing the AhR to varying degrees when compared to the endogenous level in the parental H16 HMEC. The AhR expression levels in these clones range from a 30% to an ~20-fold increase compared to the vector control (Figure 1). Two of these clones (clones A & E) exhibited a remarkable change in their morphology, with a loss of their typical epithelial shape and adoption of a more elongated fibroblastic-like pattern (Figure 2). Western blot analysis (Figure 1) revealed that clone A and clone E also have the highest increase in AhR expression. Interestingly these clones also expressed the highest levels of vimentin, which is a fibroblast-specific marker (Figure 2).

Increased AhR expression is paralleled by enhanced nuclear translocation and transcriptional activity

Since Cytochrome P450A1 (CYP1A1) expression requires an activated nuclear AhR and the expression of CYP1A1 is a direct measurement of AhR transcriptional activity, we utilized nuclear translocation of AhR and AhR-dependent CYP1A1 expression as two independent responses of AhR functional activity. Immunocytochemical staining revealed that substantial levels of AhR are localized in the nucleus in the absence of ligand treatment when AhR is overexpressed (Figure 3B). Similarly, clones overexpressing AhR by ~ 20-fold (clones A, D, E), showed substantial levels of CYP1A1 mRNA in the absence of ligand treatment (Figure 3A). These findings are consistent with ligand-independent AhR nuclear localization, also observed in these clones, thus explaining the

constitutive activity of AhR in inducing CYP1A1 expression. Not surprisingly, TCDD treatment induced CYP1A1 expression by only two-fold in these clones, despite the 20-fold higher AhR levels. This minimal induction is expected since basal levels of CYP1A1 have been so dramatically elevated by AhR overexpression alone.

AhR overexpression increases transition to S- and G2/M phases of cell cycle

To determine the impact of AhR overexpression on the cell cycle, we evaluated the cell cycle distribution of clonal cell lines. Figure 4A provides a comparison of control cells (expressing empty vector, EV) with clone A cell line, which expresses 20-fold higher AhR level. While 80% of the cells remained in G0/G1 phase of the cell cycle in the EV control cells, only about 30% remained in G0/G1 in clones that overexpressed AhR (Fig 4.A). Panel B reports the findings for all clonal cell lines.

AhR overexpression correlates with reduced cell doubling time

In order to determine what effect the AhR-induced abrogation of cell cycle transition might have on overall cellular proliferation, doubling times for each clone compared to the EV control were determined. Only the clones with the highest AhR overexpression (clones A, D, and E) exhibited a statistically significant decrease in doubling time. These clonal cell lines had a calculated doubling time of about 25 hours based on nonlinear regression analysis of Hoechst 33258 staining data for DNA content (see Methods). In contrast the proliferation rates of clonal cell lines with no (clone C) or modest (clone B) increases in AhR expression, had a doubling time that was not significantly different from the EV-control, i.e. a calculated doubling time of about 50 hours (Figure 5).

Increased AhR expression promotes mammary epithelial cell migration and invasion

Transformed cells possess a number of functional changes that distinguish them from untransformed cells. In addition to increased proliferation and altered cell cycle regulation, transformed cells also

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could acquire the ability to invade the extracellular matrix, in part due to their enhanced migration and proteolytic activities. In order to assess these characteristics of transformation, we measured the invasive potential of each clonal cell line by determining its ability to invade matrigel matrix in vitro. Matrigel, by occluding the pores of a semi-porous membrane that bisects a cell culture well, provides a barrier that is sufficient to preclude non-invasive cells from moving from the upper to lower cell culture compartment. In contrast, invasive cells have the ability to degrade the matrigel and migrate to the underside of the membrane. As shown in figure 6, clones A, D & E manifest invasive potential that is comparable to the metastatic MT2 breast cancer cell line, which is included as a positive control (Fig 6A). Thus, approximately eighty to ninety percent of the cells from clonal lines A, D or E were invasive. Microscopic images of the underside of the membrane correlate with the percentage of invasive cells calculated (Figure 6B).

Preliminary studies using cells overexpressing AhR prior to their subcloning to individual clonal cell lines revealed that the degree of cellular migration also correlates with overall AhR expression (Figure 7) and -as expected, has a characteristic dependence on cell density. Cells overexpressing AhR exhibited an average of 1.5-fold enhanced migration compared to their empty vector-carrying controls, indicating that AhR significantly ($p < 0.05$) increased the migration ability of H16 mammary epithelial cell lines (Figure 7).

Increased AhR expression correlates with anchorage-independent growth

In order to assess the ability of the clonal cell lines to grow detached from the surface, we grew the clones in soft agar for 2 weeks and determined the extent of colony formation microscopically. As shown in Figure 8, clonal lines A, D, and E formed colonies comparable in size and number to those colonies formed by the metastatic MT2 cell line. In addition, each formed 20-25 colonies per field

compared to approximately 5 visibly single viable cells in each field for clones expressing no (clone C) or small (clone B) enhancement of AhR expression (figure 8).

Discussion

In this study we provide the first evidence that the AhR is capable of inducing tumorigenic transformation in immortalized human mammary epithelial cells. Classically, transformation is associated with genetic instability and three major classes of phenotypic changes: immortalization, aberrant growth control, and malignancy. While the parental cell line used in our studies was previously immortalized, increased AhR expression in this cell line was both necessary and sufficient to induce aberrant growth and malignant phenotypes, such as increased proliferation, changes in cell cycle regulation, enhanced migration, invasion of matrigel matrix and anchorage-independent growth.

Immortalization does not automatically result in a loss of growth control, since our cell cycle analysis showed that the immortalized parent human mammary epithelial cells (H16 or the empty vector-carrying control EV) are under stringent G1→S transition control. However, increased AhR expression appeared to release these mammary epithelial cells from the G1→S block towards a much dysregulated cell cycle leading to an accumulation of cells in the S and G2/M phases. Interestingly, the low to moderate increases in AhR expression (clones B and C) have resulted only in accumulation of cells in the S-phase, and only high AhR expressing clones (clones A, D and E) managed to transition S-phase and accumulate in the G2/M phase, suggesting an apparent requirement of a threshold level of AhR expression for S-phase transition. The failure of clones B and C to transition through S-phase was reflected in their growth rate, where their doubling times were not different from the parent cells. It is plausible that overexpressed-AhR have mediated transcriptional upregulation of the required factors for the S-phase transition, such as cyclin D/Cdk4

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and Cdk6 and cyclin E/Cdk2, resulting in hyper-phosphorylation of Rb and the subsequent release of E2F transcription factor to induce the transcription of S-phase genes. In support of such a proposal is a recent report that depletion of AhR by siRNA has resulted in a significant decrease in expression of cyclin D1, cyclin E, Cdk4, Cdk6 and Cdk2 in HepG2 cells [33], contributing to the growth inhibitory effect of AhR depletion on these cells.

The data we are reporting here on the effects of AhR in transforming HMEC do not involve its ligand-dependent activation, nevertheless the high expression of AhR in clones A, D and E was accompanied by constitutive activation of AhR as evident by its nuclear localization and transcriptional activation of CYP1A1 in absence of ligand treatment. It is not currently clear what mechanisms govern this ligand-independent activation and nuclear accumulation process, however it is conceivable that the activated nuclear species of AhR account for the difference in response between these high AhR-expressing clones and the other two clones with lower AhR expression. On the other hand, the AhR activation and nuclear localization [24] is required for the association between Rb and AhR, which is deemed crucial in the cell cycle arrest induced by the AhR agonist, TCDD [23]. To reconcile these two contradicting roles for the activated AhR in promoting cell cycle arrest and enhancing progression, two models were proposed. In one model, AhR-Rb interaction functions to repress E2F activity causing G1/S arrest, and in the other model AhR-Rb interaction acts as a transcriptional co-activator for genes encoding G1/S regulatory proteins [34]. This would entail a difference between the ligand-activated and ligand-independent-activated nuclear AhR species, where the interaction of the former with Rb will behave as a repressor and the complex of the latter with Rb will function as a co-activator. Alternatively, AhR has also been shown to directly interact with the transcription factor NF- κ B, which is known to regulate many genes involved in proliferation, transformation, and apoptosis. In human breast epithelia and breast cancer cell lines,

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there is a constitutive physical interaction between NF- κ B and AhR leading to enhanced transcription of c-myc oncogene [35]. This enhanced transcription thereby might lead to increased proliferation and transformation.

Our data are important extension of previous studies that have explored the impact of relative AhR density on cellular growth [25, 26]. For instance, a lung cancer cell line (A549) manipulated to overexpress AhR grew at a faster rate in proportion to the extent of AhR expression [26]. Conversely, Hepa-1 variant cells that express lower amount of AhR when compared to wild-type Hepa-1 cells, exhibited a delayed cell growth and longer doubling time [25]. Our data are consistent with these findings, although they are on tumor cells, as they affirm that AhR expression level correlates with enhanced cellular proliferation. In addition, we have shown that AhR overexpression alone is sufficient to induce other malignant phenotypes in addition to enhanced cellular proliferation.

Invasion potential is a good indicator for malignancy, and our invasion experiments showed that overexpression of AhR by 20-fold was capable of inducing invasiveness in immortalized HMEC, to a level comparable to the metastatic cell line. Clones overexpressing AhR but to a lesser level failed to invade the matrigel matrix in vitro, suggesting that there may be a threshold for AhR expression level required for this phenotype, as well. Noteworthy, TCDD, an AhR potent agonist which activates and subsequently down-regulates the receptor [36], was reported to inhibit the invasion activity of a metastatic breast cancer cell line [37]. The ability of AhR to induce the invasiveness in HMEC might be due to previously reported affects on matrix metallo-proteinases (MMPs) and urokinase-plasminogen activator proteases (uPA) systems [38-42].

The most striking effect of the ectopic overexpression of AhR in these HMEC was the transformation of two of the clones from their typical epithelial shape into fibroblastic-like morphology. This epithelial-fibroblast transformation was accompanied by profuse expression of the fibroblast-

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associated intermediate cytoskeleton protein, vimentin. This epithelial-fibroblast transformation resembles the epithelial-mesenchymal transition (EMT), one of the hallmarks of cancer progression. Transforming growth factor beta (TGF- β) is a major player in EMT, and it is well-documented that AhR has a direct effect on TGF- β expression [38, 41, 43-46].

Classically this receptor was viewed in the context of its role in mediating the toxic and biochemical responses to environmental PAH [3, 47]. The contribution of AhR to PAH-induced carcinogenesis is well characterized through its role in the transcriptional activation of a battery of genes including *CYP1A1* and *CYP1A2* [48]. The protein products of these genes catalyze the bioactivation of some endogenous and exogenous chemicals into reactive metabolites that form DNA adducts thus contributing to the initiation of pre-neoplastic lesions [49]. Our research investigated and provided evidence for a role for AhR in the progression of breast carcinoma. This novel role for AhR is independent of ligand activation, therefore this work is distinct from, although it complements the studies using constitutively active AhR [50]. These studies report that transgenic mice expressing constitutively active AhR exhibited severe tumors of the glandular part of the stomach [50] and acquired higher susceptibility to development of hepatocarcinoma in response to treatment with a liver carcinogen [51]. Although no ligand for AhR was involved, the constitutively active AhR was generated by deletion of the ligand-binding domain to mimic the agonist-activated receptor [52], therefore it is likely that the pathway involved is via the transcriptional induction of CYPs and bioactivation with the subsequent cancer initiation. Our study, on the other hand addressed the basic question of whether AhR itself has the potential of acting as a proto-oncogene and as a factor capable of advancing the progression of breast carcinoma and our data have provided some support for this claim.

Conclusion

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Although the precise molecular mechanism requires further investigation, the present data suggest that AhR has an oncogenic potential and contributes to the progression of breast cancer from pre-cancerous cells to malignant invasive carcinoma. Such a property might not be unique for the breast and might accompany tumor progression in other target organ/system. Thus the data identify AhR as a relevant therapeutic target for cancer treatment.

Abbreviations

AhR, aryl hydrocarbon receptor; ARNT, aryl hydrocarbon receptor nuclear translocation protein; CYP1A1, cytochrome P450 1A1; CYP1B1, cytochrome P450 1B1; bHLH, basic helix-loop-helix; HMEC, human mammary epithelial cell line; PAH, polyaromatic hydrocarbons; TCDD, 2,3,7,8-tetrachlorodibenzo-p-dioxin; FACS, fluorescence activated cell sorter; Rb, retinoblastoma; cdk, cyclin-dependent kinase; EV, empty vector.

Competing interest

The authors declare that they have no competing interest.

Authors' contributions

SEE conceived the study. JB and SEE designed the study. JB performed collection of data and statistics. JB and SEE drafted the manuscript. All authors read and approved the final version of manuscript.

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FIGURE LEGENDS

FIGURE 1.

Analysis of AhR protein expression in AhR-transformed H16N2 clones compared to their empty vector (EV) control.

A. Western immunoblotting analysis. Five clones (A-E) with varying levels of AhR-expression and a clone expressing only the empty vector (EV) were isolated by limiting dilution from G418-selected transformed H16N2 cell lines. Ten μ g of protein from each clone was analyzed by Western immunoblotting. Upper panel is a representative blot and lower panel is the densitometric quantitation of AhR protein (apparent molecular mass of 108 kDa) in the clones. Values in the graph are means and standard deviations of n=3 independent cultures of different analyses. Values from different experimental analyses were each normalized internally to the respective EV control before the mean and SD was calculated.

B. Immunocytochemical staining of AhR protein expression in H16 clones. Clones were grown on coverslips and fixed with methanol: acetone. AhR was visualized by staining with rabbit anti-AhR polyclonal antibodies followed by a rhodamine-conjugated donkey anti-rabbit. Images were captured on an Olympus fluorescence microscope (200x magnification). Lower panels are the phase contrast images of the cells.

FIGURE 2.

Immunocytochemical staining for vimentin in clones of H16 mammary epithelial cells

A. Western immunoblotting analysis

Ten μ g of protein from each clonal cell line was analyzed by Western blotting. Illustrated is a representative blot of vimentin protein expression (apparent molecular mass of 58 kDa) in the clones.

B. Immunocytochemical staining for Vimentin expression in H16 clones

Appendix 9

Clonal cell lines were grown on coverslips and fixed with methanol: acetone. Cells were immunostained for vimentin by incubating with a 1:50 dilution of mouse anti-vimentin monoclonal antibodies (clone V9, from Sigma Chemicals) followed by FITC-conjugated donkey anti-mouse antibodies. The nuclei were counter-stained with DAPI fluorescence dye. Cell images were captured by an Olympus fluorescence microscope (1000x magnification), and images from DAPI and FITC-fluorescence channels were merged. As a positive control, human mammary fibroblasts (HMF) were stained. Clone A cell line was stained as a negative control by eliminating primary antibody.

FIGURE 3.

A. RT-PCR analysis of CYP1A1 mRNA expression in H16 Clones overexpressing AhR. Cells were treated with 1 nM TCDD or vehicle (DMSO) for 24h and total RNA was isolated and subjected to reverse transcriptase (RT) reaction, as described in the methods section. RT products were subsequently used for semi-quantitative PCR amplification of CYP1A1 and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was amplified simultaneously as an internal control. Upper panel is a representative image of ethidium bromide-stained gel of PCR products of clones. The intensity of bands was quantified by digital imaging and normalized to GAPDH signals. The means and standard deviations of duplicate PCR of three independent experiments were plotted in graph in lower panel.

B. Subcellular localization of AhR in H16 clones by immuno-cytochemical staining. Clones were grown on coverslips and fixed with methanol: acetone. AhR was visualized by staining with rabbit anti-AhR polyclonal antibodies followed by a rhodamine-conjugated donkey anti-rabbit. Images were captured on an Olympus fluorescence microscope (500x magnification). Clones with the highest

AhR-overexpression have substantial AhR levels localized to the nucleus in absence of ligand treatment

FIGURE 4

Cell Cycle Distribution of AhR-overexpressing clonal cell lines of H16N2. Cells were fixed in 70% ethanol, stained with propidium iodide, and analyzed by fluorescence-activated cell sorting (FACS) analysis as described in the methods section. The percentage of cell cycle distribution was determined using ModFit analysis software. The upper panel is a representative histogram, comparing clone A to the EV control clone. The lower panel is a table summarizing the percentage distribution of cells among different phases of cell cycle. The values in table are means and standard deviations of two independent cultures, each analyzed in duplicates.

FIGURE 5

Population doubling times of AhR-overexpressing clones compared to their vector control.

Cells were grown in 96 well plates for 3, 12, 24 and 48 hours. They were then lysed and the DNA stained with Hoechst 33258 nucleic acid dye. Fluorescence was measured (in Artificial Fluorescence Units AFU, which were correlated to cell numbers) using excitation and emission wavelength 360nm and 460nm, respectively. Cell numbers were plotted against time using Graphpad statistical software and doubling times were calculated by non-linear regression curve analysis (for exponential growth). Values in graph are average population doubling times of the clonal cell lines. Values are means and standard deviations of triplicate determination of three independent experiments. (*) denotes significant difference from the EV control ($p < 0.05$).

FIGURE 6

A. Analysis of invasive potential of AhR-transformed clones of H16N2 cells. Cell suspensions (2.5×10^4) of normal or AhR over-expressing cells were plated in BD FluoroBlok invasion chambers containing matrigel, and incubated for 24 hours. Cells passing to the underside of the insert were stained with calcein AM fluorescence dye. Calcein fluorescence of invasive cells was measured on Cytofluor at excitation/emission wavelengths 485/530nm respectively. The fluorescence of the invasive cells was calculated as a percentage of the fluorescence of total cells. A. Values plotted are the means and standard deviations of three independent experiments, where each experiment was run in duplicate. (*) denotes significant difference from EV control ($p < 0.05$)

B. Microscopic images of invasive cells. Representative microscopic images of invasive cells were taken at 10X magnification following staining with calcein AM of the underside of the insert.

FIGURE 7.

Effects of overexpressed AhR on migration of H16 mammary epithelial cells.

The migration measurements were done using the BD FluoroBlok chambers without matrigel. Cell suspensions were prepared by trypsinizing cell monolayers and resuspending the cells in serum free media at 5×10^4 cells/ml. Medium (750ul) containing 5% fetal calf serum was added to the bottom of each well as a chemo-attractant. A 500ul aliquot of the cell suspension (at three cell densities) was added to the top chamber. The cells were incubated at 37°C for 24 hours. Following incubation, the media from the top chamber was carefully removed by aspiration and the insert was transferred to a second plate containing 0.5ml/well of 4µg/ml Calcein AM (Molecular Probes, Eugene, OR). The plates were allowed to incubate for 1 hour at 37°C. Calcein fluorescence of the migrating cells was

read at excitation and emission wavelength of 485 and 530 respectively. Symbols denote significant difference ($p < 0.05$) from the respective EV control of different cell density.

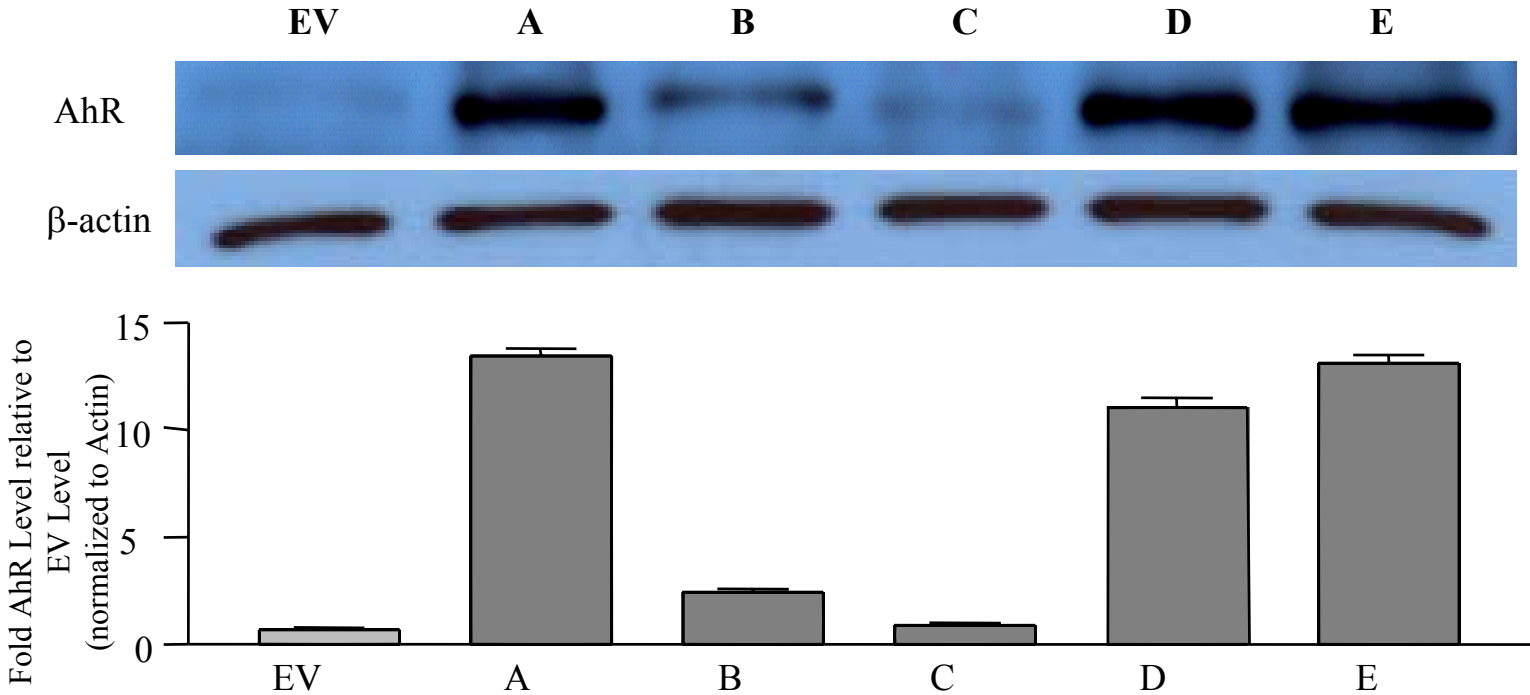
FIGURE 8.

Anchorage-independent growth of AhR-over-expressing clones of H16N2 in soft agar.

Cell suspensions of different clones were prepared in 0.3% agar media and overlaid onto 0.6% agar layer coated on each well of the six-well plates. Cells were plated in triplicate at two cell densities. Individual cells were visualized microscopically and colony formation was monitored for up to 2 weeks. The numbers of colonies were counted at low magnification (20x) and the scoring was done by three independent observers. Values are means and standard deviations of two independent experiments. (*) is significantly different from EV control ($p < 0.05$).

Figure 1

A.



B.

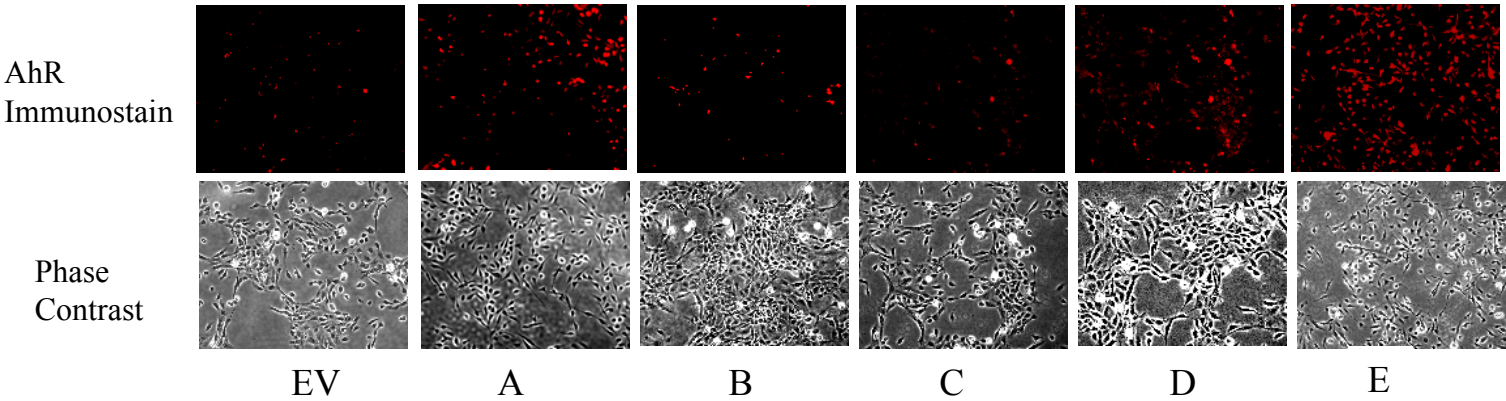


Figure 2

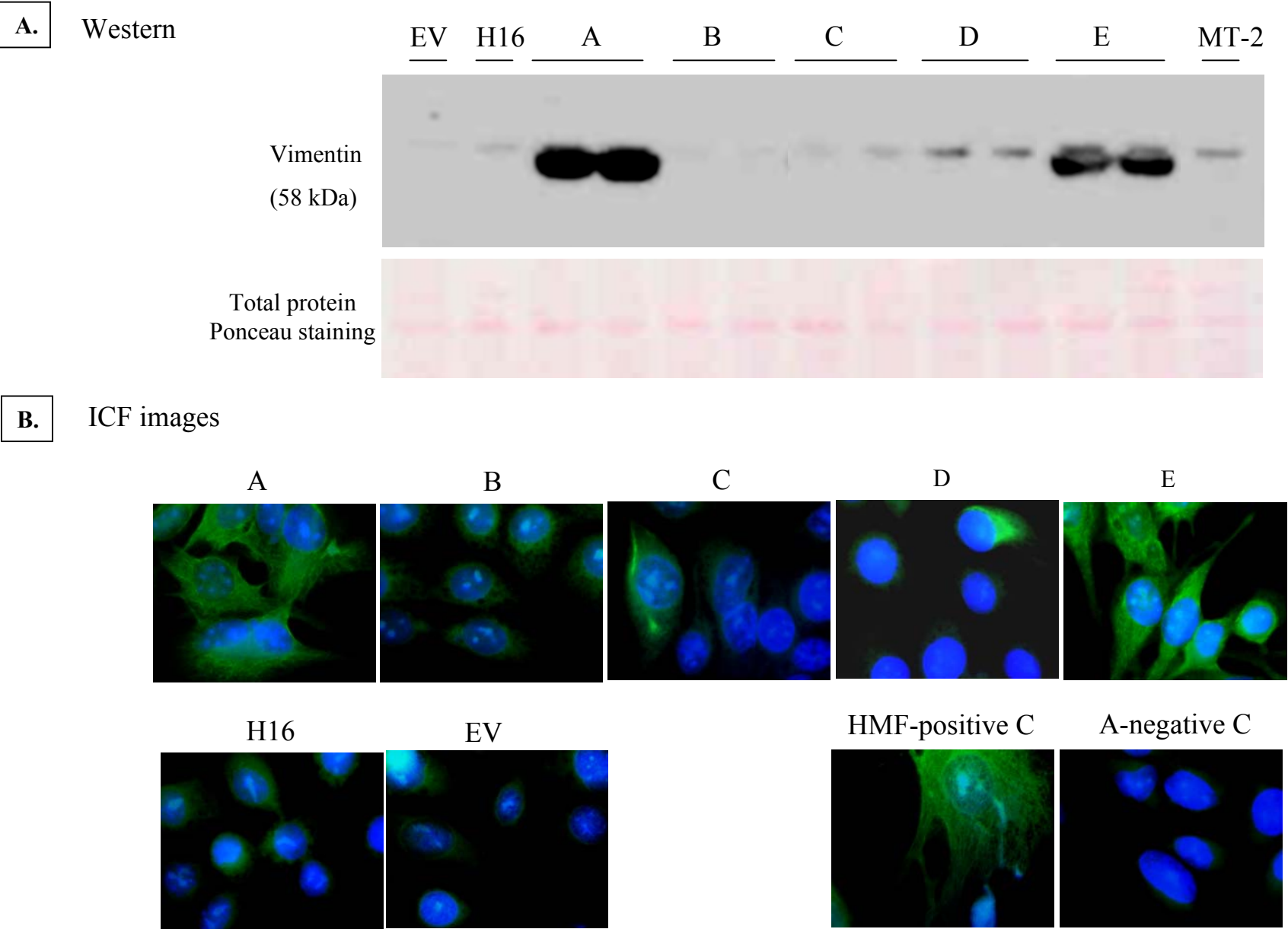
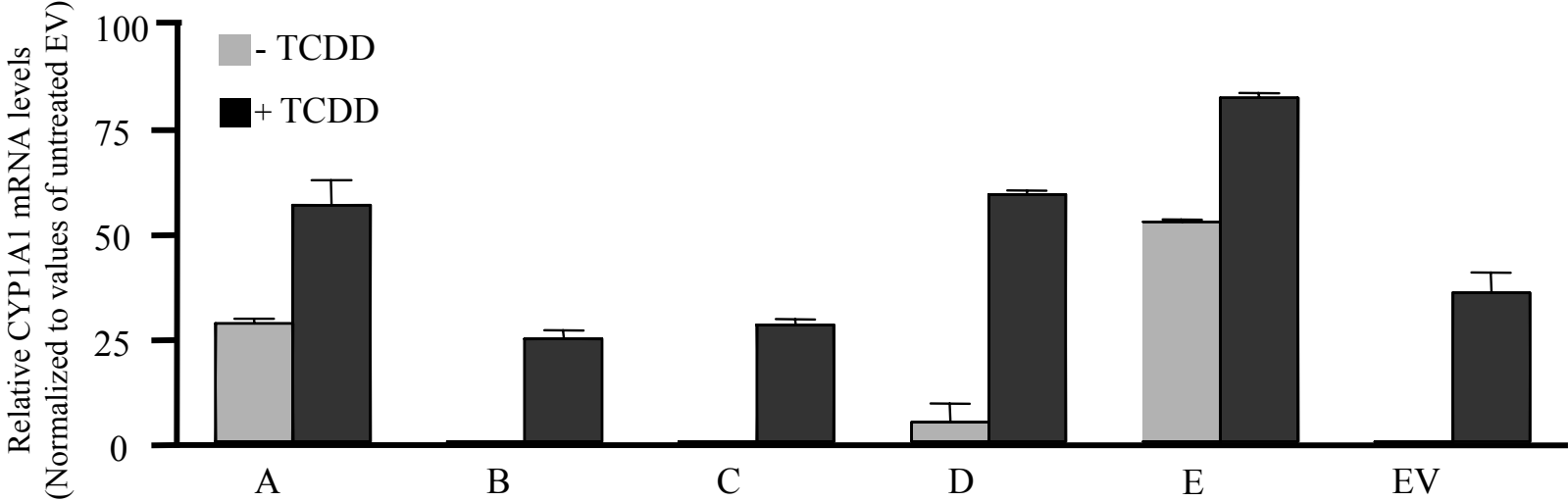
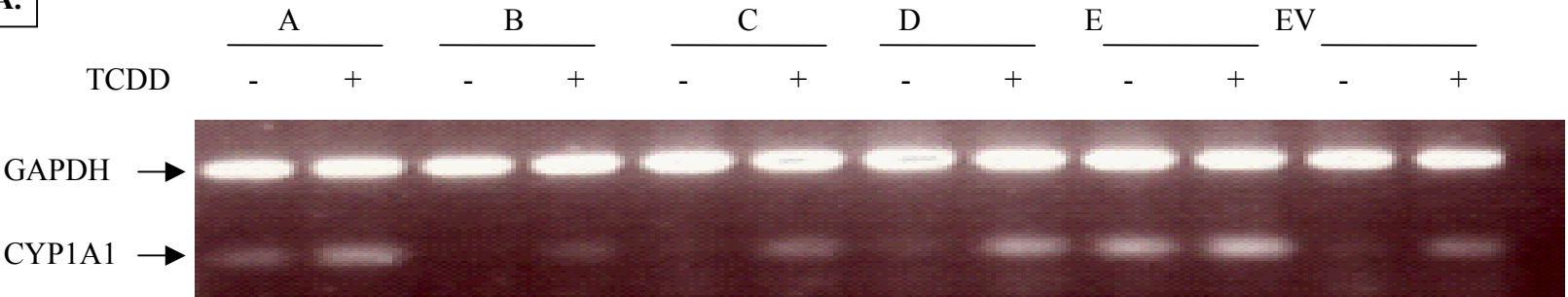


Figure 3

A.



B.

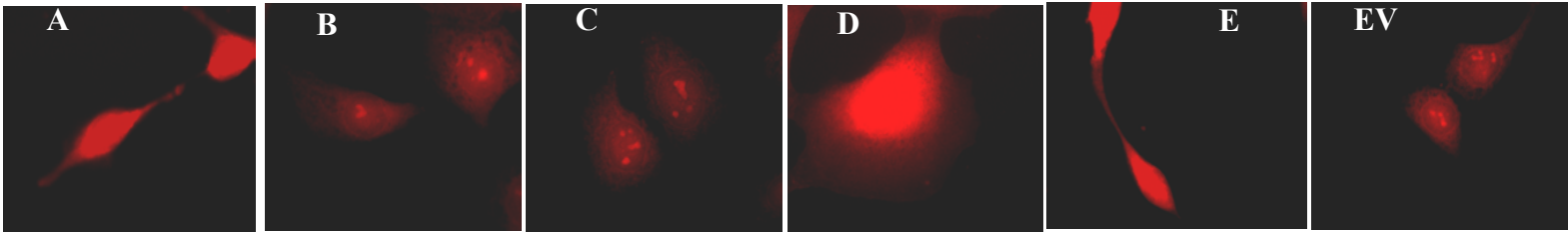
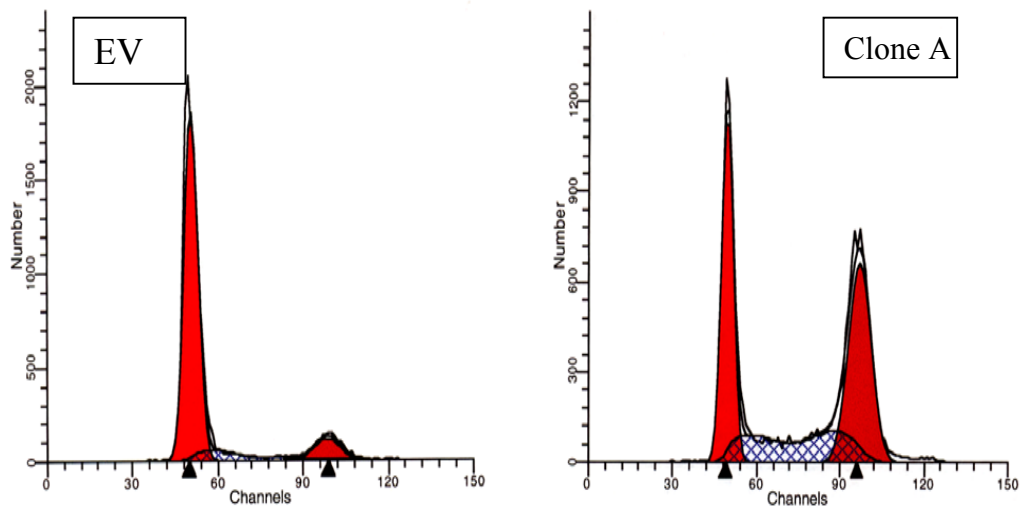


Figure 4



	G0/G1	S-PHASE	G2/M
A	32.44 +/- .46	35.23 +/- .35	32.31 +/- .11
B	60.95 +/- 1.78	27.25 +/- 1.2	11.81 +/- .57
C	50.36 +/- 2.79	35.55 +/- 2.051	14.09 +/- .74
D	31.32 +/- .07	36.32 +/- 1.18	32.37 +/- 1.19
E	31.78 +/- .04	36.60 +/- 1.202	31.62 +/- 1.16
EV	80.37 +/- .75	10.775 +/- .785	8.86 +/- .05

Figure 5

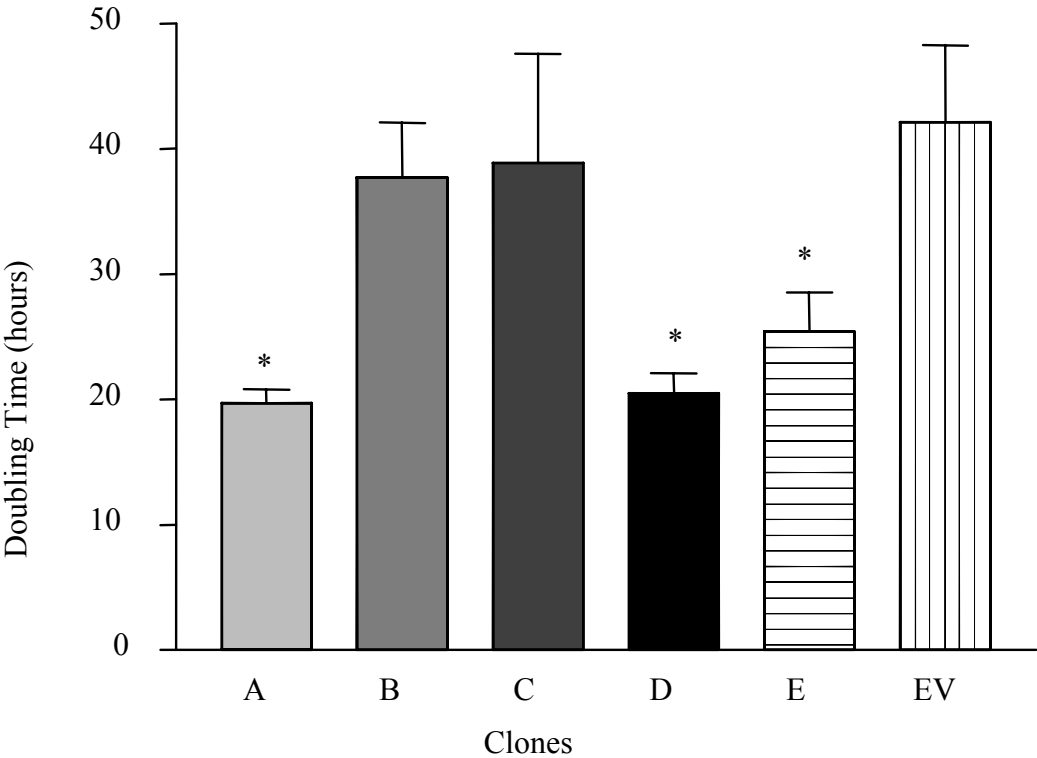


Figure 6

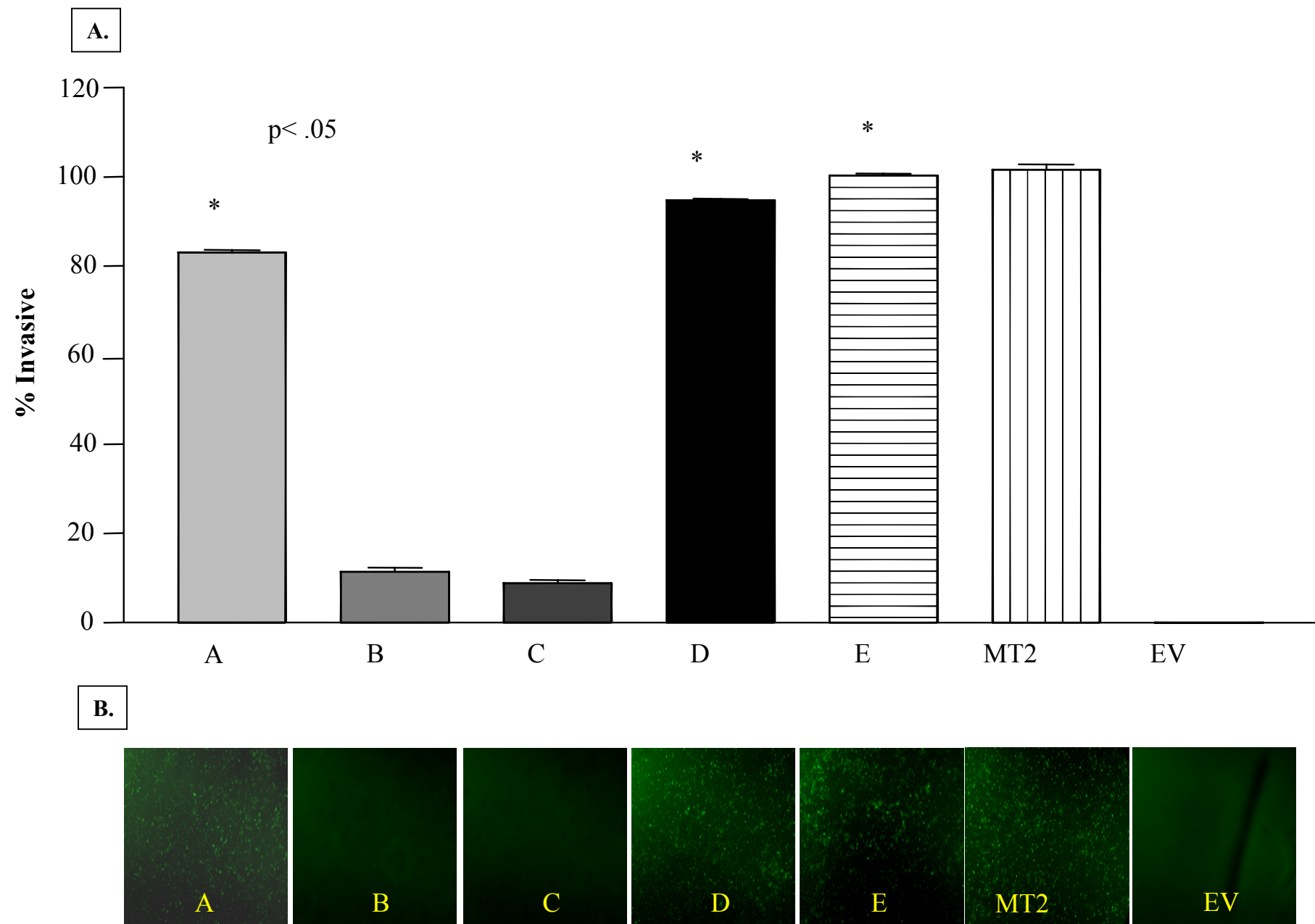


Figure 7

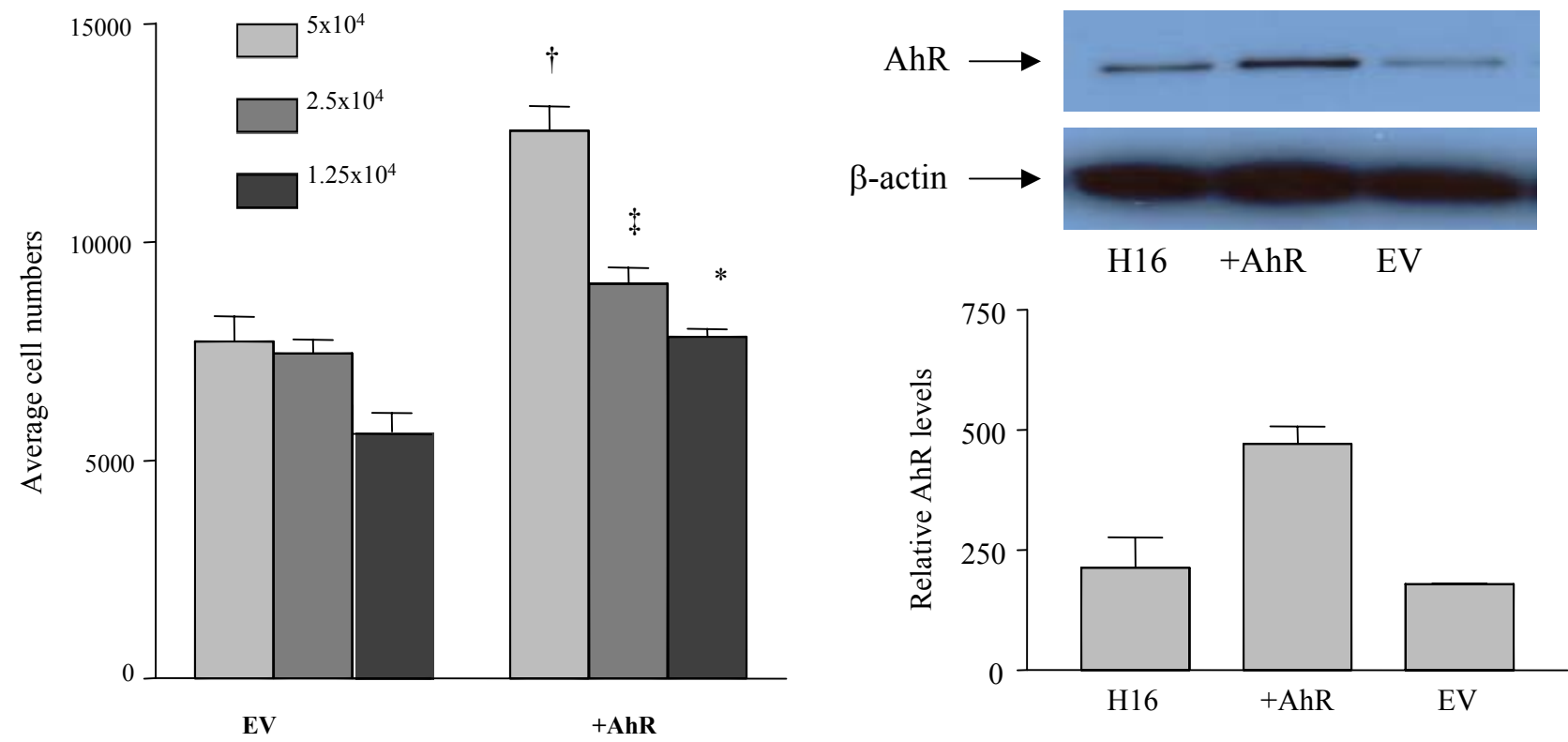


Figure 8

